

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 15:54:59 ; Search time 1605.5 Seconds  
(without alignments)  
7599.656 Million cell updates/sec

```

Title:      US-09-733-507-1
Perfect score: 904
Sequence:   1 atctctctctcacagaga.....tatgttttggtagcagata 904

```

SCORING TABLE: IDENTIFICATION

Gapop 10.0 , Gapext 1.0

```
Searched:      13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
1: em_esta:*
2: em_estim:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_astro:*
8: em_hnc:*
9: gb_estli:*
10: gb_estl2:*
11: gb_hnc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vrt:*
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## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	293.8	32.5	352	10	T88456	T88456_12152_Lambda
2	272	30.1	329	10	T21659	T21659_3667_Lambda
3	146.4	16.2	503	12	B78433	B78433_127E12T1.1
4	102.2	11.3	1101	12	CNS00396	AL0654921_Drosophila
5	85.8	9.5	997	12	CNS00507E	AL0676767_Drosophila
6	80.6	8.9	1101	12	CNS0162P	AL108811_Drosophila
7	77.8	8.6	987	12	CNS000418	AL0656337_Drosophila
8	74.4	8.2	689	10	BM436539	BM4365399_VA003E050
9	68.6	7.3	1101	12	CNS00039G	AL0654921_Drosophila
10	66	7.3	77	9	AM004548	AM004548_701932225
11	65	7.2	585	10	BG643706	BG643706_EST119001
12	64.8	7.2	1101	12	CNS0088WC	B56547706_Drosophila
13	64.6	7.1	938	12	CNS0102F	AL098443_Drosophila
14	63.6	7.0	1201	12	CNS0107R	AL098623_Drosophila
15	63.4	7.0	908	12	BH136237	BH136237_ENTRV47E
16	63.2	7.0	1101	12	CNS000D1	AL065414_Drosophila
17	63	7.0	510	10	B1129591	B1129591_G092P90Y

C	18	62.6	6.9	996	12	CNS00FPH	AL071063 Drosophila
C	19	62	6.9	987	12	CNS01APC	AL104456 Drosophila
C	20	61.8	6.8	1101	12	CNS016CX	AL098695 Drosophila
C	21	61.6	6.8	938	12	CNS006CJ	AL065806 Drosophila
C	22	61	6.7	1125	9	AL547503	CNS006CJ
C	23	60.8	6.7	914	12	CNS002ZY	AL097768 Drosophila
C	24	60.6	6.7	623	10	BE347049	sp34c09.y
C	25	60.4	6.7	928	12	CNS00DKY	AL071865 Drosophila
C	26	60	6.6	617	12	AZ296172	AL091612 RPT-23-1
C	27	60	6.6	668	12	AZ312109	AZ312109 1M0027K13
C	28	59.6	6.6	1101	12	CNS003BR	AL063332 Drosophila
C	29	59.6	6.6	1101	12	CNS00EVL	AL069706 Drosophila
C	30	59.6	6.6	1101	12	CNS017XE	AL108152 Drosophila
C	31	59.2	6.5	1101	12	CNS0021J	AL061336 Drosophila
C	32	59	6.5	1001	12	CNS0155H	AL105023 Drosophila
C	33	58.8	6.5	846	12	CNS000KV	AL078250 Drosophila
C	34	58.6	6.5	1101	12	CNS00EWC	AL070972 Drosophila
C	35	58.6	6.5	1204	12	CNS016P2	AL106628 Drosophila
C	36	58.4	6.5	896	12	CNS00DB8	AL057462 Drosophila
C	37	57.6	6.4	585	12	AZ060400	AZ060400 RPT-23-4
C	38	57.6	6.4	1030	12	CNS021P3	AL203088 Tetradon
C	39	57.2	6.3	777	12	CNS025WB	AL182612 Tetradon
C	40	57.4	6.3	821	12	CNS033FF	AL241332 Tetradon
C	41	57.2	6.3	1101	12	CNS00P66	AL070820 Drosophila
C	42	57.2	6.3	1101	12	CNS017S5	AL108706 Drosophila
C	43	57	6.3	620	10	BE823380	BE823380 GM7000198
C	44	57	6.3	1101	12	CNS0100X	AL098379 Drosophila
C	45	56.4	6.2	424	10	BI503896	BI503896 BHI70025A

RESULT	1
788456	
LOCUS	
DEFINITION	788456 352 bp TRNA linear EST 09-JAN-1998
ACCESSION	12155 Lambda-PRL2 Arabidopsis thaliana cDNA clone 15622417, mRNA
VERSION	188456
KEYWORDS	sequence.
SOURCE	188456.1 GI:936292
ORGANISM	EST.
	thale cress.
	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE	1 (bases 1 to 352)
AUTHORS	Neman, T., deBrujin, F.J., Green, P., Keester, K., Kende, H., McIntosh, L., Ohlrooge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
TITLE	Gene galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones
JOURNAL	Plant Physiol. 106, 1241-1255 (1994)
MEDLINE	95148729
COMMENT	On Apr 14, 1993 this sequence version replaced gi:716808.

```

FEATURES
  source
    location/Qualifiers
      1..352
        /organism="Arabidopsis thaliana"
        /strain="var Columbia"
        /db_xref="taxon:3702"
        /clone="156J2417"
        /clone_1fp="Lambda-PR12"
        /note="Vector: Lambda zip-lox; Site_1: Sal; Site_2: NotI"
        /lambda_PRI1="A cDNA library derived from equal

```

quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-lox. The cDNA inserts were directionally cloned with Sal-Not arms using 0.190 dt primed cDNA. 84 t 14 others

BASE COUNT 112 a 48 c 94 g 84 t 14 others  
ORIGIN

Query Match 32.5%; Score 293.8; DB 10; Length 352;  
Best Local Similarity 88.3%; Pred. No. 9.1e-38;  
Matches 310; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

16 agagattgtaacttcacgacacgtaacctaatcgaagaatggtgagaaatagaaaa  
1 AGAGATTGTAACCTACGACACGTAACCTAAATCGAAGATGGTGAGAAATATAGAAA  
60

76 gctaaaggaattgagaagcgtgaggttcgaacgcatatgagctcagagccggaga  
61 NCTAAAGGAATTNTAGAGGCTGGAGTTTCGTAACGTAATNCAAGCTACGAGCCGGAGA  
120

136 attgttatgttagatcggaaaaatcaagctctgctccgctcgctgataatgagtt  
121 ATTGTTATNTNAGATCGGAAATCAAGCTCTGCTCGCTCGGTGATATGAGATT  
180

196 tgcgtcgtcttagtggaaagcaatgatatagaagaagaataatcactctggaggg  
181 TCGTGCTCTTAGTGGAGCAAGANTATAGAGAAAGANTTAATACCTCTGGAGAG  
240

256 gaagataaagatcggtgacacgtaacgctgacgtacgaagggtgagaaaggaagct  
241 GAAGATAAAGATGCGTGAACACTGAACGTCGACGTATGCCGGGGTAGCGAGAGAGCTT  
300

316 ttggaatactcgagaagagaggaagaagaataaagtaaccatcgatgag 366  
301 TTTNNAAAATCTNTGNNAGAGGCTGAANAGGTTTAGTATCCCTTGCG 351

RESULT 2 329 bp mRNA linear EST 07-JAN-1998  
T21659  
LOCUS T21659  
DEFINITION 3667 Lambda-PRL2 Arabidopsis thaliana cDNA clone 96D157, mRNA  
sequence.  
ACCESSION T21659  
VERSION T21659.1 GI:2757169  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 329)  
Newman,T., deBruin,J.F., Green,P., Keegstra,K., Kende,H., McIntosh  
,L., Ohlrogge,J., Raike,N., Somerville,S., Thomasow,M., Retzel  
,E. and Somerville,C  
Genes galore: a summary of methods for accessing results from  
large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
Plant Physiol. 106, 1241-1255 (1994)  
95148729  
On Jan 7, 1998 this sequence version replaced gi:914567.  
Contact: Thomas Newman  
MSU-DOE Plant Research Laboratory  
Michigan State University  
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.  
Lansing, MI  
Tel.: 517-353-0854  
Fax: 517-353-9168  
Email: 2213tcn@lhm.cl.msu.edu  
Seq primer: T7.  
Location/Qualifiers

source 1. 329  
/organism="Arabidopsis thaliana"  
/strain="var columbia"  
/db\_xref="taxon:3702"  
/clone="96D157"  
/clone="11b="Lambda-PRL2"  
/note="vector: Lambda Zip-lox; Site-1: Sal; Site-2: Not;  
Lambda PRL2 is a cDNA library derived from equal  
quantities of 4 pools of mRNA. The mRNA sources were 1) 7  
day germinated etiolated seedlings; 2) tissue culture  
grown roots; 3) staged plants half with 24 hour light  
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)  
same plants as 3 but aerial tissue (stems, flowers and  
siliques. The vector is BRL's lambda Zip-lox. The cDNA  
inserts were directionally cloned with Sal-Not arms using  
0.190 dt primed cDNA. 82 t 13 others

BASE COUNT 106 a 50 c 78 g 82 t 13 others  
ORIGIN

Query Match 30.1%; Score 272; DB 10; Length 329;  
Best Local Similarity 94.7%; Pred. No. 2.9e-34;  
Matches 286; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

1 atctctctctcacagagattgtaacttcacgacacgtaacctaatcgaagaatg-t 59  
1 ATCTCTCTCTCTCACAGAGATTGTACTTCACGACACGTAACCTAAATCGAAGATGNT 60

60 gagaaatatagaagaagcctaaggaattgtaagaagctggaagttcgtaacgtatatga 119  
61 GAGAAATATNTAGAAACCTAAAGGAATGTGAAGCTGGAGTTTCCTCAACGTATATNCA 120

120 gctcagagccggagaattgttatgtaactcggaaaaaatcaagctctgctccgtgt 179  
121 GCTNCGGAGCCGGAGATTTGTTATGTTAAGNCGGAAATCAAGCTCTGCTCGTGT 180

180 cgtgataatggaattcgctcgtctgttagtgaagcaatgaatatagaagaagaatt 239  
181 CGGTGATATNTGNTTCATCGCTCTTGTATGTGGACCAATGAATNTAANNNAAGANT 240

240 aatacatctggagaggaagaatgaatggtgacgtgacgtgacgtgacgtgacgtg 299  
241 AATACATCTGGGGGAGAGAGATTAAGATGCTGACACTGAACGCTGCACATATCNGCGTT 300

300 ga 301  
301 NA 302

RESULT 3 503 bp DNA linear GSS 16-JAN-1998  
B78431  
LOCUS B78431  
DEFINITION T27E12F.1 TAMU Arabidopsis thaliana genomic clone T27E12, DNA  
sequence.  
ACCESSION B78431  
VERSION B78431.1 GI:2775070  
KEYWORDS GSS.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 503)  
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golden,K.  
,Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter  
,J.C.  
A BAC End Sequence Database for Identifying Minimal Overlaps in  
Arabidopsis Genomic Sequencing. Update 3  
Unpublished (1997)  
Other GSSs: T27E12F.1 T27E12F.2 T27E12F.3  
Contact: Steve Rounsley  
Department of Eukaryotic Genomics  
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: rounslay@ligr.org  
 Seq primer: M13-21  
 Class: BAC ends  
 High quality sequence stop: 503.

# FEATURES

Location/Qualifiers

1..503

/organism="Arabidopsis thaliana"

/db\_xref="taxon:3702"

/clone="T27E12"

/clone\_lib="TAMU"

/sex="hermaphrodite"

/note="Vector: BelosAclII; Site\_1: HindIII; Site\_2: HindIII"

; Produced by Rod Wing"

BASE COUNT 163 a 122 c 77 g 140 t 1 others

## ORIGIN

Query Match 16.2%; Score 146.4; DB 12; Length 503;  
 Best Local Similarity 98.7%; Pred. No. 3.5e-14;  
 Matches 147; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atctctctctcaccgagattgttaacttcacgcacacgttaacttaactgaagatgtg 60

Db 355 ATCTCTCTCTCACGAGATTGTGACTTCACGACACGTAACTCAATCGAATGCTG 414

QY 61 agaaaatagaaaagcctaagaattgtgaagctgtgagcttcgtcaacgtatagcag 120

Db 415 AGAAATATAGAAAAGCTAAGCAATTGTGAGAGCTGAGTTGCTCAAGTATATGAG 474

QY 121 ctacgagccgagagattgtttatgttag 149

Db 475 CTACGAGCCGAGAGATTGTATGTATGTTAG 503

## RESULT

4

CNS00396/c

LOCUS

DEFINITION

1101 bp DNA linear GSS 03-JUN-1999

Drosophila melanogaster genome survey sequence TET3 end of BAC #

BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

AL063921

AL063921.1 GI:4941778

GSS.

fruit fly.

Drosophila

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

Bp 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osogawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

Ecotri digestion of Drosophila DNA provided by the BDGP from the

isogenic strain Y2; on bw sp. the same strain used for the BDGP's

p1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

# FEATURES

Location/Qualifiers

1..1101

/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"

/clone\_lib="RPCI-98"

/clone="BACR08K10"

/note="end : TET3"

BASE COUNT 201 a 64 c 131 g 202 t 503 others

ORIGIN

Query Match 11.3%; Score 102.2; DB 12; Length 1101;  
 Best Local Similarity 20.4%; Pred. No. 3.4e-07;  
 Matches 167; Conservative 324; Mismatches 322; Indels 4; Gaps 2;

QY 78 taagaagtgtgagaagctcgagcttcgtcaacgtatagctacgagccgagaat 137

Db 1100 KARRMGDDTWDRDTRKDDMDTKMTWKDRADBRNAGDADRNAMDDGAGTMTATMMW 1041

QY 138 tgttatgttagatcgaaatacaagctcgtccgtcgctcggtgataatgagtttc 197

Db 1040 WWWWATWDTWMDKMMWATAKTDTATWMTWTRADWAGRDGAKRRDADADGA 981

QY 198 gtgcgtcttgtagtggaagcaat-gaataagaagaagaattatcatctggaagag 256

Db 980 GRDGRKRRKDKDKDKDDDKGKKKKAKAKAKAAMWAKWMDMDKMDKMDAKRKA 921

QY 257 aagataaagatgtgtacacatcgaaacgtcgaatcgaggtgacgaagaagaagctt 316

Db 920 DDDGAGDDKDDGKDDDDDDTGTGKDDDDKDDMDKMDKAGTGDTWMAATDMMW 861

QY 317 tgaagaatcgagaagagagagagaagaattaaagaatcacaatgaaatattcat 376

Db 860 WADADMTWDAADWADWADWADWADWADWADWADWADWADWADWADWADWADW 801

QY 377 cgaatttgaatcgagctgaaagaatcgttagattgttgttagcggaggaagaaga 436

Db 800 RKRADKRDADRDADRDADRDADRDADRDADRDADRDADRDADRDADRDADRD 741

QY 437 tgaagagagacggtgacgagagagagagagagagagagagagagagagagag 436

Db 742 -DAGTAGGKMRTRMRKRRDTRWDADADTRADRRRRGGDADAGGKTKRRR 664

QY 497 cgaatcgaagaattgaagaattttttgtggaagctgagaagaacacgaagaagaatca 556

Db 683 RDRBATWDRDAMWADAWMTTDTFTDMDKRDGRKRGARRRTTARAAMDWTKAW 624

QY 557 agagaagatcaatctgatttcgagaagaagcattgaagaagcattgaagaagc 616

Db 623 DWAKMDWKRADRMWADWTDARADRWAKARARARARARARARARARARAR 564

QY 617 taaagttagagtgagaagaagaagaagttatggttttttttttttttttttttttt 676

Db 563 TTAATWTTMAARAAMWMAATTTATWTTTWTWTTTWTWTTTWTWTTTWTWTTT 504

QY 677 aatattcagaagaataaattatatttctgtgatttgaagaataaattgttga 736

Db 503 ATWAAATTAAMWAAAAAATTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTT 444

QY 737 ggaatttttttgaagaagaattgacacagaagaagaagaagaagcttttaacagattt 796

Db 443 TTTTWTWTTWMAATTTATTTTWTWTTWTTWTTWTTWTTWTTWTTWTTWTT 384

QY 797 agagccagagaagaagctgctttagcttaacttcaactctctcttgaactgtgta 856

Db 383 CCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 324

QY 857 tcttttagatattctttagatattttagattttagattttagattttagattttagattt 893

Db 323 YYYYYYYCCCTCNCNCYYCCCTTTCYTTT 287

## RESULT

5



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QY 206 gtagtgagcaatgataataagaagaataatacatctgagaggagaataag 265
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 545 GMEKAKGAAGGGRGGRBVGNGRDATATATATAAADDTKRWBARGAATAAADA 604
QY 266 atggtcaacctaaacgtcgatcgagggtagaagaagaagcttttgaatc 325
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 605 RWAAKWTWAAAAAARAAAAAATAAAGTTTAAATAAAGGKGKGAADGD 664
QY 326 tgaagaagaagaagaagaataagtaataatccatgagaatattcatcggaattg 385
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 665 GGAATAADARRGRRGRRRAAARAADAATAAATAAATAAATAAAGKRRKWK 724
QY 386 aatcgcggttaagaatctgttagatctgttgtagcggagagaagaatgaga 445
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 725 GDCXDCGKATKTAAMAKGRKDWGTATAMWTWATWADTWAKATDADAKAAGRRKRDAR 784
QY 446 cgtgacggcggagagagagaggaatgagtagcggagagtagcgaacgcg 505
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 785 KTRADGRRARRRRRAAAGKRAAAGARRAARAADDDRDMAAATAAATAA 844
QY 506 aatgaagaattt-ttggagaagctgagaacaactcaagaataatcaagaaga 564
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 845 TWRDRWMDWDMDTFRMDDTTAAWWDARARARRRRRRARRRAARAADDDTK 904
QY 565 tacaattcgattcgagaagaagagccatagaagaagcttaagaatgagtt 624
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 905 DRWADATTKDVTKTWTTDDDDWAKRRWMAAADAAMWRDARADMAATAKDDGW 964
QY 625 gaagagaagaagaagaagttatgatttttttttaacttttagatttaatttc 684
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 965 KDWGGRGRRGGRKRRWKXGKTGKDDDDWKTWRDMMWMTTKKDDMMWDGRRGR 1024
QY 685 aaggaaatgaatattttttgtgatttgaataatgaatttgaagaagaatg 744
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 1025 WTKRKGAWWRADAWARDITDGTADKRRKTDTKRGDDWRKDRKRRDKGD 1084
QY 745 ttgaagaagaat 761
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 1085 DKTKKATWDDDDARDW 1101
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |

RESULT 7
CNS00418/c 987 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence Tm3 end of BAC #
DEFINITION BACR09C16 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL066537.1 GI:4942778
VERSION AL066537
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscocomphla; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 987)
AUTHORS Direct Submission
TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazuhiro Osegaawa and
Aaron Mammser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library

```

```

FEATURES
    source
        /organism="Drosophila melanogaster"
        /db_xref="taxon:7227"
        /clone_1db="RPCI-98"
        /clone="BACR09C16"
        /note="end : Tm3"
BASE COUNT 238 a 162 c 17 g 177 t 393 others
ORIGIN
Query Match 8.6%; Score 77.8; DB 12; Length 987;
Best Local Similarity 25.6%; Pred. No. 0.0029;
Matches 112; Conservative 134; Mismatches 191; Indels 0; Gaps 0;

QY 208 agtgaagaatgataataagaagaataatacatctgagagagaagaataag 267
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 916 ARARAAARAAARARARARARARARARARARARARARARARARARARAR 857
QY 268 ggtgacactgaacgtgcgacgtatcgagggtagcgaagaagctttgaaatcg 327
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 856 RRRGRRGRRGRRGRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 797
QY 328 agagaagagagaagaagaatgaataatccatgagaatattcatcgaaattgaa 387
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 796 RGRGRRGRRGRRGRRGRRGRRGRRGRRGRRGRRGRRGRRGRRGRRGRR 737
QY 388 tggcggttaagaatctgttagatgtgtgtgtgtagcggagagaagaatgagaag 447
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 736 AARARAAARARARARARARARARARARARARARARARARARARARAR 677
QY 448 gtagcggcggagagagagagagcgaattgtagcggagatccacaggaatcgaa 507
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 676 RGRARRRRGRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 617
QY 508 atgaagaattttttgtgaaagctgagaacacaccgaagaataatcaagaagaatc 567
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 616 RRRGRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 557
QY 568 aattcgattcgagaagaagacatagaagaagcttaagaatgagttgag 627
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Db 556 GRRGRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 497
QY 628 tgaagaagaagaag 644
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |
Db 496 RRAARAAAGAAGARAG 480
| : : | | | : : | | | : : | | | : : | | | : : | | | : : |

RESULT 8
BMA36399 689 bp mRNA linear EST 31-JAN-2002
LOCUS VVA003E05.52381 An expressed sequence tag database for abiotic
DEFINITION stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera
CDNA clone VVA003E05.5, mRNA sequence.
ACCESSION BMA36399
VERSION BMA36399.1 GI:18458121
KEYWORDS EST.
SOURCE Vitis vinifera.
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 689)
AUTHORS Cramer G.R. and Cushman J.C.
TITLE An expressed sequence tag database for abiotic stressed leaves of
JOURNAL Vitis vinifera var. Chardonnay
CONTACT: Cushman JC
UNPUBLISHED (2002)
JOURNAL Department of Biochemistry
COMMENT University of Nevada

```



Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P.,  
Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R.,  
Rose, M., Warren, B., Top, B., Kastury, K., Borillo, C., Carpio, T.,  
Pollock, J., Suzuki, G., Argentine, C., Shah, S., Nobrega, A., Murry, L.,  
Turner, C., Kirkorian, S., Elder, L., and Hanson, D.  
Arabidopsis thaliana Gene Expression Microarray  
Unpublished (1999)

JOURNAL  
COMMENT  
Contact: David Smoller, Ph.D.  
Genome Systems, Inc., a wholly owned subsidiary of Incyte  
Pharmaceuticals, Inc.  
4633 World Parkway Circle, St. Louis, MO 63134, USA  
Tel: 877-577-2733  
Fax: 314-427-3324  
Email: service@genomesystems.com.

FEATURES  
source  
Location/Qualifiers  
1..77

/organism="Arabidopsis thaliana"  
/db\_xref="taxon:3702"  
/clone="70193225"  
/clone\_lib="A. thaliana, mixed source"  
/note="this sequence was obtained from a clone generated  
with a PCR product of the target gene."  
BASE COUNT  
17 a 19 c 12 g 29 t  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Pired. No. 0.42;  
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 752 gtagcaattgcacagaaagaaagccttttaacagatttagagcccaagaatg 811  
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Db 66 gtagcaattgcacagaaagaaagcctttttacagatttagagcccaagaatg 7

QY 812 cgtgtc 817  
|||||  
Db 6 cgtgtc 1

RESULT 11  
Bg643706 585 bp mRNA linear EST 24-APR-2001  
LOCUS  
DEFINITION EST11900 tomato shoot/meristem Lycopersicon esculentum cDNA clone  
CTOP32610 5' sequence, mRNA sequence.  
ACCESSION Bg643706  
VERSION Bg643706.1 GI:13778931  
KEYWORDS EST.  
SOURCE tomato.  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Asterales; euasterids I; Solanales; Solanaceae; Solanum;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Lycopersicon.  
1 (bases 1 to 585)  
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Uterback, T.,  
Hansen, C., Rohnig, C. and Tanksley, S.  
Generation of ESTs from tomato shoot/meristem tissue  
Unpublished (2001)  
Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES  
source  
Location/Qualifiers  
1..585

/organism="Lycopersicon esculentum"  
/cultivar="TA96"  
/db\_xref="taxon:4081"  
/clone="CTOP32610"  
/clone\_lib="tomato shoot/meristem"  
/tissue\_type="shoot/meristem"  
/dev\_stage="developing shoots from 4-6wks old plants"  
/lab\_host="SOLR"

/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2:  
XhoI; Small expanding leaves from the growing tip were  
taken from greenhouse plants (4-6wks old TA96). Tissue  
was immediately frozen in liquid nitrogen."  
BASE COUNT  
193 a 108 c 144 g 140 t  
ORIGIN

Query Match  
Best Local Similarity 67.2%; Pired. No. 0.37;  
Matches 92; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 490 atgcacaaggaatcggaaatgtgaatttttctggaagctggaacaactcaagaa 549  
|||||  
Db 240 ATCCCAAGAGATCTTGAATGAGAGCTTTTACCCGTGACAGAAAGAGCAGACAGA 299  
QY 550 aaattcagaagaagtaaatctgatttcgaagaagaagccattgaagagcttcc 609  
|||||  
Db 300 AAATTCATCGAGAACTTCACTTGTATCCAGTGAACGAGAGCCCTTCCGGACCTTAC 359  
QY 610 gaatggtaaaagttaga 626  
|||||  
Db 360 GAATGGGTGCAAGTAA 376

RESULT 12  
CNS008WC/C 1101 bp DNA linear GSS 03-JUN-1999  
LOCUS  
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BACR18L14 of RPCL-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL052719  
VERSION AL052719.1 GI:4934268  
KEYWORDS GSS.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT  
Direct Submission  
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the Berkeley Drosophila Genome Project (BDGP).  
The BDGP is constructing a physical map of the Drosophila  
melanogaster genome using these BACs. For further information  
please see <http://www.fruitfly.org> The BDGP Drosophila  
melanogaster BAC library was prepared by Kazutoyo Googawa and  
Aaron Mammoser in Pieter de Jong's laboratory in the Department of  
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
NY. The library is named RPCL-98 and was constructed by partial  
EcoRI digestion of Drosophila DNA provided by the BDGP from the  
isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
p1 and EST libraries. A more detailed description of the library  
and how to order individual BAC clones, the entire library, or  
filters for hybridization from the BACPAC Resource Center can be  
found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source  
Location/Qualifiers  
1..1101

/organism="Drosophila melanogaster"  
/db\_xref="taxon:7227"  
/clone\_lib="RPCL-98"  
/clone="BACR18L14"  
/note="end : TET3"  
BASE COUNT  
145 a 171 c 122 g 340 t 323 others  
ORIGIN

Query Match  
Best Local Similarity 7.2%; Score 64.8; DB 12; Length 1101;  
31.5%; Pired. No. 0.34;

Matches 128; Conservative 102; Mismatches 165; Indels 11; Gaps 1;

Qy 382 ttgagtcgagcgttaaagaatcgttagatgttctgttagcggaggaacacatgag 441  
 Db 1001 TMTTWTTRTAGKTDGADAKKTKMKADGDTGTGGCGTGGANGAATWTKRKGKGG 942  
 Qy 442 gagaagtcgacgagcggagagagagaagaacgaattgacgcgagatgcacagaa 501  
 Db 941 RKGDGGRGKGGGGGGGGMGWRKGMWTKGAGGGGKGMWTKAGKATGAGGKGM 882  
 Qy 502 tcgagaattgagaattttctgtgaagctgagaacaactcaagaacaaatcaagaag 561  
 Db 881 GGTGTATTWTAATWTRWMAWRTWWRRRATWAMWTTTKTATTAATAAKAMWWRK 822  
 Qy 562 aagtaacattcgcattcgcagaagagaagccattagaagacgttaccgaatggttaag 621  
 Db 821 AATATWATATWMTTATTTATTAAGRARAWMTAAWATTAARATWAMWWRRAAT 762  
 Qy 622 ttagagtcgaagaagaagaagatttgcgttgcgttttttttttttttttttt 670  
 Db 761 TTAATAAARAAAMDAWATWTTATDWTTTAATRAAADKATTTTATTTATWTT 702  
 Qy 671 gatttaatttcaggaggaatgaattatttctgttagattggaatataaagatt 730  
 Db 701 GTTTTATWTTGTTTGTTRKRWTKRRRTTGTTRATRTTTTKKMAWTTTATWTT 642  
 Qy 731 gtagagaagaatgtttttagaagtcgaatgcacagaagaagaag 776  
 Db 641 TTGGTTGRRRDATTGAATAAATAAATAAATAAATAAATAAATAAATAAATAA 596

RESULT 13  
 CDS0102F/c 928 bp DNA linear GSS 26-JUL-1999  
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC  
 DEFINITION BACN03B09 of DrosBAC library from Drosophila melanogaster (fruit  
 fly); genomic survey sequence.  
 ACCESSION AL098433  
 VERSION AL098433.1 GI:5610044  
 KEYWORDS GSS.  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 928)  
 REFERENCE Genoscope.  
 AUTHORS Direct Submission  
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage  
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT - Web : www.genoscope.cns.fr  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the European Drosophila Genome Project (EDGP) -  
 http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC  
 library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
 d'Etude du Polymorphisme Humain) with funding provided by a MRC  
 project grant. The DNA was prepared from embryos by Alain Bucheton  
 and Genevieve Payan. It has been constructed in the vector  
 pBelobAC11.

#### FEATURES

source Location/Qualifiers  
 1..928  
 /organism="Drosophila melanogaster"  
 /plasmid="pBelobAC11"  
 /db\_xref="taxon:7227"  
 /clone\_lib="DrosBAC"  
 /clone="BACN03B09"  
 /note="end : 17"  
 BASE COUNT 169 a 128 c 100 g 241 t 290 others  
 ORIGIN

Query Match 7.1%; Score 64.6; DB 12; Length 928;  
 Best Local Similarity 25.1%; Pred. No. 0.38;

Matches 146; Conservative 183; Mismatches 247; Indels 5; Gaps 3;

Qy 210 tggagcaatcaataaagaagaatttaacatctcggagaggaatgaatgag 269  
 Db 926 WGTAAAGKAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAG 867  
 Qy 270 tgacacgtgaacgctgcagcgtatcgcagcgtgacgaagaagcgttttgaacatcag 329  
 Db 866 AARATATKAKGTGTRWGAATRADKDDGTGTGWTGWRGKRRRAGDGTGDR 807  
 Qy 330 agagaagaagaagaagaatttaagtaacatcagcgaatttaacatcgaattgaac 389  
 Db 806 TTRTRAGKAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAGWAG 747  
 Qy 350 ggcggttaagaacatcgttagattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 449  
 Db 746 TATTAMWWRWRDRRAATGTGKWTGTTTAKAGATGGMDDTGA-DARKRAAGTTATKT 688  
 Qy 450 gacgcgaggaagaagaagaagcgaattgagcagcagatgcacagcgaatcgaat 509  
 Db 687 ATATGTAKDRKAK 628  
 Qy 510 tgaagattttctgtgaagctgagaacaacacacacacacacacacacacacacac 569  
 Db 627 AGWTGKWTGDKWRKKTDRATGWRATATW--AGAADAWADGWRAGTGAARRWDGW 571  
 Qy 570 ttgcatttcgagaagaagaagccattagaagaagcgttaccgaatggttaagtcg 629  
 Db 570 RWRARADTRKAGAADRAGAAAAAGTGTGAADAKRAARKGKDDGKRKTKGAAG 511  
 Qy 630 aagaagaagaagaagatttgcgttttttttttttttttttttttttttttttttt 689  
 Db 510 GWRGAGRAKDDDKRGWGMKRRKAKDKTKTKWTRIDKAKAKAKAKAKAKAKAKAK 450  
 Qy 650 ataagtaatt 749  
 Db 451 RKKGCGGAGATATGTGWMWMTATGATATGATATGATATGATATGATATGATATG 392  
 Qy 750 aagtaagaattgcacagaagaagaagaagcgttttaaca 790  
 Db 391 ARAAMGAAAAAKGAK 351

RESULT 14  
 CDS0107R/c 1201 bp DNA linear GSS 26-JUL-1999  
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC  
 DEFINITION BACN03G13 of DrosBAC library from Drosophila melanogaster (fruit  
 fly); genomic survey sequence.  
 ACCESSION AL098625  
 VERSION AL098625.1 GI:5610236  
 KEYWORDS GSS.  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 1201)  
 REFERENCE Genoscope.  
 AUTHORS Direct Submission  
 TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage  
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

COMMENT - Web : www.genoscope.cns.fr  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the European Drosophila Genome Project (EDGP) -  
 http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC  
 library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
 d'Etude du Polymorphisme Humain) with funding provided by a MRC  
 project grant. The DNA was prepared from embryos by Alain Bucheton  
 and Genevieve Payan. It has been constructed in the vector  
 pBelobAC11.

FEATURES  
 source Location/Qualifiers  
 1..1201





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 15:54:59 ; Search time 47.3 Seconds  
(without alignments)  
4694.560 Million cell updates/sec

Title: US-09-733-507-1

Perfect score: 904  
1 atctctctctcacagaga.....tatgtttgtgactgata 904

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 38353 segs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCrUS.COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	92.6	10.2	7218	1 US-08-232-463-14	Sequence 14, Appl
2	47.8	5.3	289	4 US-09-007-005-17	Sequence 17, Appl
3	47.8	5.3	289	4 US-09-244-796-17	Sequence 17, Appl
4	43.6	4.8	16442	3 US-08-781-891-208	Sequence 208, App
5	42.8	4.7	19124	2 US-08-487-8268-13	Sequence 13, Appl
6	42.4	4.7	19124	2 US-08-487-8268-13	Sequence 13, Appl
7	42.4	4.6	4526	1 US-07-855-412B-4	Sequence 4, Appl
8	42.4	4.6	4526	2 US-08-308-887A-4	Sequence 4, Appl
9	42.4	4.6	4526	3 US-08-881-094-4	Sequence 4, Appl
10	41.8	4.6	7832	4 US-09-004-838-94	Sequence 94, Appl
11	41.4	4.6	1669	4 US-09-461-697-184	Sequence 184, App
12	41.2	4.6	5852	1 US-07-867-106-2	Sequence 2, Appl
13	41.2	4.5	1365	1 US-07-807-043B-4	Sequence 4, Appl
14	41.2	4.5	1365	1 US-08-299-849B-4	Sequence 4, Appl
15	41.2	4.5	1365	2 US-08-147-368A-4	Sequence 4, Appl
16	41.2	4.5	1365	3 US-08-967-727-4	Sequence 4, Appl
17	41.2	4.5	1365	4 US-08-037-230D-4	Sequence 4, Appl
18	40.8	4.5	1654	3 US-08-913-842-20	Sequence 20, Appl
19	40.8	4.5	1744	3 US-08-913-842-27	Sequence 27, Appl
20	40.8	4.5	1875	3 US-08-913-842-1	Sequence 1, Appl
21	40.8	4.5	1965	3 US-08-913-842-2	Sequence 2, Appl
22	40.4	4.5	1972	1 US-08-463-048-1	Sequence 1, Appl
23	40.4	4.5	1972	1 US-08-463-229-1	Sequence 1, Appl
24	40.4	4.5	1972	2 US-08-302-891-1	Sequence 1, Appl
25	40.4	4.5	51259	3 US-08-781-891-209	Sequence 209, App
26	39.8	4.4	10968	2 US-08-680-337-2	Sequence 2, Appl
27	39.8	4.4	10968	4 US-09-228-246-1	Sequence 1, Appl

C 28	39.6	4.4	1117	4 US-09-247-3735-33	Sequence 33, Appl
29	39.4	4.4	2255	4 US-08-871-5728-3	Sequence 3, Appl
C 30	39.4	4.4	5506	4 US-09-004-838-93	Sequence 93, Appl
31	39.2	4.3	599	4 US-09-328-111-147	Sequence 147, App
32	39.2	4.3	1298	3 US-08-948-705-3	Sequence 3, Appl
33	39.2	4.3	273	2 US-08-737-298-1	Sequence 1, Appl
34	39.2	4.3	3211	2 US-08-574-959A-8	Sequence 8, Appl
35	39.2	4.3	3211	4 US-09-357-014-8	Sequence 6, Appl
36	39.2	4.3	3901	2 US-08-574-959A-6	Sequence 6, Appl
37	39.2	4.3	3901	4 US-09-357-014-6	Sequence 6, Appl
38	39.2	4.3	5852	1 US-07-867-106-2	Sequence 2, Appl
39	38.8	4.3	243	1 US-08-182-175A-56	Sequence 56, Appl
40	38.8	4.3	243	1 US-08-474-633A-74	Sequence 74, Appl
41	38.8	4.3	243	5 PCT-US92-06412-56	Sequence 56, Appl
42	38.8	4.3	1276	4 US-09-177-325-2	Sequence 2, Appl
43	38.8	4.3	1276	4 US-09-411-812A-2	Sequence 2, Appl
44	38.8	4.3	1276	4 US-09-590-113-2	Sequence 2, Appl
45	38.8	4.3	6243	2 US-09-056-075-1	Sequence 1, Appl

# ALIGNMENTS

RESULT 1  
US-08-232-463-14/C  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHNEIFLINGER, F.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)836-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pT5gt-F15  
US-08-232-463-14

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Query Match 5.3%; Score 47.8; DB 4; Length 289;
Best Local Similarity 9.8%; Pred No. 0.0067;
Matches 24; Conservative 101; Mismatches 120; Indels 0; Gaps 0
QY 316 ttggaatcgtgagagagaggaagaagaaatgaagtaatcattgagaattatca 375
      . . . . . . . . . . . . . . . . . . . . . . . . . . . .
Db 42 uuaatcacaatuuatgrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrrr 101

```

[illegible]



```

1      FILING DATE: 03/19/92
2      CLASSIFICATION: 536
3      ATTORNEY/AGENT INFORMATION:
4      NAME: Smith, Dean F.
5      REGISTRATION NUMBER: 36,683
6      REFERENCE/DOCKET NUMBER: 75500002
7      TELECOMMUNICATION INFORMATION:
8      TELEPHONE: (810) 641-1600
9      TELEFAX: (810) 641-0270
10     TELEX: 287637 Harnes UR
11     INFORMATION FOR SEQ. ID NO.: 4:
12     SEQUENCE CHARACTERISTICS:
13     LENGTH: 4526 bases
14     TYPE: nucleic acid
15     STRANDEDNESS: single
16     TOPOLOGY: linear
17     MOLECULE TYPE: DNA
18     DESCRIPTION:  prosystemlin genomic DNA; Figures 8A-8C.
19     US-07-855-412B-4
20
21     Query Match          4.6%; Score 42; DB 1; Length 4526;
22     Best Local Similarity 47.4%; Pred. No. 0.43;
23     Matches 126; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
24
25     Oy 622 tttagagtcgaagaagaagaagatttagtcttttttttaacttttagatttaatat 681
26     Db 2306 TGAGTATGAGAGAGTACTTAAATTCCTTCCTTGACTTTATTTATTTATTTTGTATAT 2365
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28     Oy 682 ttcaggaataaattatttttttttttttttttttttttttttttttttttttttt 741
29     Db 2366 TTTACGTCTCATTTATTTATTTATTCACAAATTAATTTATTCACATTAATTTCTTTAT 2425
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31     Oy 742 gtcttagaagtagcaaatctgcacgaaaaagaagaagcttttaacagatttagagc 801
32     Db 2426 TTTCTCAAAATTCACAGAGAAATATGAAAAAGAAAAATTAAGTTAAAAAAGAGCTCAG 2485
33
34     Oy 802 ccgaaagtcgtgtcttttttttttttttttttttttttttttttttttttttttt 861
35     Db 2486 CCAAGATTCACACAAAGATTAATCATATATCTCATATGAGCTTAAGATTTATTTTCT 2545
36
37     Oy 862 tagcatctcttagacattttat 887
38     Db 2546 TCTTATTTTCATATATTTTATTTT 2571
39
40     RESULT      8
41     US-08-308-887A-4
42     Sequence 4, Application US/08308887A
43     Patent No. 5863076
44     GENERAL INFORMATION:
45     APPLICANT: Ryan, C.A.
46     APPLICANT: Mousul, B.F.
47     APPLICANT: Pearce, G.L.
48     TITLE OF INVENTION: "SYSTEMIN"
49     NUMBER OF SEQUENCES: 8
50     CORRESPONDENCE ADDRESSES:
51     ADDRESSEE: Harnes, Dickey & Pierce, P.L.C.
52     STREET: P.O. Box 828
53     CITY: Troy
54     STATE: Michigan
55     COUNTRY: USA
56     ZIP: 48303
57     COMPUTER READABLE FORM:
58     MEDIUM TYPE: Diskette-5.25 inch, 1.2MB storage
59     COMPUTER: IBM PC/386 Compatible
60     OPERATING SYSTEM: MS-DOS 4.01
61     SOFTWARE: Word for Windows-7
62     CURRENT APPLICATION DATA:
63     APPLICATION NUMBER: US/08/308,887A
64     FILING DATE: September 19, 1994
65     CLASSIFICATION: 435
66     ATTORNEY/AGENT INFORMATION:

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NAME: Smith, DeAnn F.  
REGISTRATION NUMBER: 36,683  
REFERENCE/DOCKET NUMBER: 755500001USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 641-1600  
TELEFAX: (810) 641-0270  
TELEX: 287637 Harnes UR  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4526 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
DESCRIPTION: prosystemin genomic DNA; Figures 8A-8C.  
US-08-308-887A-4

Query Match 4.6%; Score 42; DB 2; Length 4526;  
Best Local Similarity 47.4%; Pred. No. 0.43;  
Matches 126; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 622 tttagagtgaaagaagaagaagtttagtttttttttaacttttagatttaaat 681  
DB 2306 TGAATATGAGAGAGTAACTTAAATTTCTTTGACTTTTATTAATTTTGTATAT 2365  
QY 682 tttagagtgaaagaagaagaagtttagtttttttttaacttttagatttaaat 741  
DB 2366 TTTACTGTCTATTTATTTTCAATATTCACAAATTAATTTATTCACATATATGCTTTATT 2425  
QY 742 gtttttagaagtcgaagattgcacagaagaagaagaagcttttaacagatttaagagc 801  
DB 2426 TTTCTCAAAATTTACAGAACATATGAAAAAGAAATAGTTGAAAAAGACACCCATC 2485  
QY 802 ccaagaagtcgctgtcttagctttagctttagctttagctttagctttagctttagctt 861  
DB 2486 CCAAGATATCAACACAAAGTATATCTATCTATCTATCTATCTATCTATCTATCTATCT 2545  
QY 862 tagcatattcttagatattttat 887  
DB 2546 TCTATTTTTCATATATTTTATT 2571

RESULT 9  
US-08-881-094-4  
Sequence 4, Application US/0881094A  
Patent No. 6022739  
GENERAL INFORMATION:  
APPLICANT: Ryan, Clarence A  
APPLICANT: Pearce, Gregory L  
APPLICANT: McGill, Barry F  
TITLE OF INVENTION: Systemin  
FILE REFERENCE: 7555-000001CPB  
CURRENT APPLICATION NUMBER: US/08/881,094A  
CURRENT FILING DATE: 1997-07-09  
EARLIER APPLICATION NUMBER: 08/308,887  
EARLIER FILING DATE: 1994-09-19  
EARLIER APPLICATION NUMBER: PCT/US93/02428  
EARLIER FILING DATE: 1993-03-18  
EARLIER APPLICATION NUMBER: 07/885,412  
EARLIER FILING DATE: 1992-03-19  
EARLIER APPLICATION NUMBER: 07/528,956  
EARLIER FILING DATE: 1990-05-25  
EARLIER APPLICATION NUMBER: PCT/US91/03685  
EARLIER FILING DATE: 1991-05-24  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 4  
LENGTH: 4526  
TYPE: DNA  
ORGANISM: Lycopersicon esculentum  
US-08-881-094-4

Query Match 4.6%; Score 42; DB 3; Length 4526;  
Best Local Similarity 47.4%; Pred. No. 0.43;  
Matches 126; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 622 tttagagtgaaagaagaagaagtttagtttttttttaacttttagatttaaat 681  
DB 2306 tttagagtgaaagaagaagaagtttagtttttttttaacttttagatttaaat 2365  
QY 682 tttagagtgaaagaagaagaagtttagtttttttttaacttttagatttaaat 741  
DB 2366 tttagagtgaaagaagaagaagtttagtttttttttaacttttagatttaaat 2425  
QY 742 gtttttagaagtcgaagattgcacagaagaagaagaagcttttaacagatttaagagc 801  
DB 2426 ttcttaaaatttcaggaagaataagaaagaagaagtagttgaaagagctcacc 2485  
QY 802 ccaagaagtcgctgtcttagctttagctttagctttagctttagctttagctt 861  
DB 2486 ccaagatatacaacaagaagatatacatatcttcaatgccaagattttattct 2545  
QY 862 tagcatattcttagatattttat 887  
DB 2546 tcttattttcatattattttatt 2571

RESULT 10  
US-09-004-838-94  
Sequence 94, Application US/09004838  
Patent No. 6350933  
GENERAL INFORMATION:  
APPLICANT: Michelmore, Richard W.  
APPLICANT: Shen, Kathy  
APPLICANT: Meyers, Blake  
TITLE OF INVENTION: Procedures and Materials for  
TITLE OF INVENTION: Conferring Pest Resistance in Plants  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/004,838  
FILING DATE: 09-JAN-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/781,734  
FILING DATE: 10-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Einhorn, Gregory P.  
REGISTRATION NUMBER: 38,440  
REFERENCE/DOCKET NUMBER: 023070-078810US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7832 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY:  
LOCATION: 1..7832



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Db	5453	TTTTTAAATAATCAATATTTAAATAATTAATCTATATATCTTGATGACTCTCAATTT	5394
Qy	730	tgtagaaggaatgcttttagaagtaagatgcacagaataagaagaagcttttaac	789
Db	5333	TATTAATTTAATATTTAATTTTAAAAATTAAGTATCATGAGCTATATATTTTCCA	5334
Qy	790	agattttaga	799
Db	5333	TGTTTTTAAA	5324

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Query Match	4.58;	Score 41;	DB 1;	Length 1365;
Best Local Similarity	50.28;	Pred. No. 0.48;		
Matches 101; Conservative	0;	Mismatches 100;	Indels 0;	Gaps 0;

[illegible]

Db 1110 GGGAAACCCGGATGGCTTTCACCTTAGGCGATGCATGCCAAGCCCAAGAAAGAAAT 1169  
 QY 630 aagaagaagaagaaggttlaagtttttttttlaactctttagatttaatttaattcaagga 689  
 Db 1170 GGACAGGGGGAAGAGTGTGTTTTTTTTTCCCTTCATTAATTCTAGTATTGTA 1229  
 QY 690 ataagttcaattatttctgt 710  
 Db 1230 TCCAGAAATTTGATTTTGT 1250

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RESULT 14
US-08-299-849B-4
: Sequence 4, Application US/08299849B
: Patent No. 5612201
: GENERAL INFORMATION:
: APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
: APPLICANT: Lelh, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
: APPLICANT: Chomez, Patrick
: TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
: TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
: NUMBER OF SEQUENCES: 48
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Felfe & Lynch
: STREET: 805 Third Avenue
: CITY: New York City
: STATE: New York
: ZIP: 10022
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
: COMPUTER: IBM
: OPERATING SYSTEM: PC-DOS
: SOFTWARE: Wordperfect
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/299, 849B
: FILING DATE: 1-SEPTEMBER-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/037, 230
: FILING DATE: 26-MARCH-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/04354
: FILING DATE: 22-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/807, 043
: FILING DATE: 12-DECEMBER-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/764, 364
: FILING DATE: 23-SEPTEMBER-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/728, 838
: APPLICATION NUMBER: 9-JULY-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/705, 702
: FILING DATE: 23-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Hanson, No. 561201man D.
: REGISTRATION NUMBER: 30, 946
: REFERENCE/DOCKET NUMBER: LUD 5355
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 688-9200
: TELEFAX: (212) 838-3884
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1365 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: genomic DNA
US-08-299-849B-4

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Query Match	4.58;	Score 41;	DB 1;	Length 1365;
Best Local Similarity	50.28;	Pred. No. 0.48;		
Matches 101;	Conservative 0;	Mismatches 100;	Indels 0;	Gaps 0;

QY	510	tgaagattttttt	gtgaagctgaagaaacac	ccaagaagaattccgaagaactaca	569
Db	1050	TGAAGAGCTTGC	ATGGAAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAAAT		11079
QY	570	tttcgatttcga	aagaaagacccattagaagcgttc	agaaatggttaagtagtg	629
Db	1110	GGGAAACCCGG	ATGGCTTCTCACCTTAGGCATTCGAAATTCGAAAGCCCAAGAAAGAAAGAAAT		11659
QY	630	aagaaagaaaga	aagatttagtcttttttttaactctt	taatttaatttaattcaagga	689
Db	1170	GGACAGCGGGA	GAGAGTGCTGTTTCTTTTCCCTTCATTAATTTCTAGTTTATGATA		12259
QY	690	ataagttattcat	tattattgtg	710	
Db	1230	TCCAGAAATTTG	ATTTTGT	1250	

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RESULT 15
US-08-142-368A-4
; Sequence 4, Application US/08.442368A
; Patent No. 5925729
; GENERAL INFORMATION:

```

ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

```

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
3
4 COMPUTER: IBM
5
6 OPERATING SYSTEM: PC-DOS
7
8 SOFTWARE: Wordperfect
9
10 CURRENT APPLICATION DATA:
11
12 APPLICATION NUMBER: 05/08/142.366A
13
14 FILING DATE: 02-MAY-1994
15
16 CLASSIFICATION: 435
17

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PROR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PROR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PROR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PROR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
APPLICATION NUMBER: 9-JULY-1991
PROR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 592572man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253,4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ. ID NO.: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1365 base pairs
type: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-08-142-368A-4

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	Query Match	Best Local Similarity	Matches	Score 41	Pred. No.	Mismatches	DB 2	Length	Indels	Gaps
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Oy	510	tgaagatttttttgytagcctgagaaacaactcaaaaaaatccaagaagatcaca	569							
Db	1050	TGAAGAGCTTGCATGCGAAGAGAGAAAGAAAGAGAGAGAGAGAGAGAGAAAT	1109							
Oy	570	tttcgatttcgaaagaagaagcctgaaagagcgttaagaatgaggttaagctagag	629							
Db	1110	GGGAACCCGCGATGGCTTCTCACCTTAAGCATGCAAGTTGCCAAACCCAGAGAAACAAT	1169							
Oy	630	aagaagaagaagaagcttaagcttttttttaactcttttagatttaactatctcgag	689							
Db	1170	GGACAGGGGAGAGAGAGGCTGTTTCTTTTTCCTCTCATTAATTTCTAGCTTTTAGTA	1229							
Oy	690	ataagttaatttcaatttgct	710							
Db	1230	TCCGAAAATTTGATTTTGTT	1250							

Search completed: September 4, 2002, 17:23:35  
Job time: 5316 sec



XX 16-DEC-1999.  
XX 08-JUN-1999; 99MO-CA00532.  
XX 08-JUN-1998; 98CA-2235978.  
XX 31-DEC-1998; 98CA-2256121.  
XX (MIAC) AGRIC & AGRI FOOD CANADA.  
XX (UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.  
XX (CANA) NAT RES COUNCIL CANADA.  
XX Wang H, Fowke LC, Crosby WL;  
XX WPI; 2000-097540/08.  
XX P-PSDB: AAY44335.  
XX Modifying plant cell development using nucleic acid encoding inhibitor  
XX of cyclin-dependent kinase, or corresponding antisense sequence, e.g.  
XX for inducing male sterility.  
XX Claim 5; Fig 1; 58pp; English.

CC The present sequence is a cDNA encoding A. thaliana Cyclin-Dependent  
CC kinase (CDK) inhibitor, ICK1. Interactor of Cdc2 kinase 1 (ICK1)  
CC interacts with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3. Growth,  
CC morphogenesis, multiplication, enlargement, differentiation and  
CC maturation of plant cells can be modified by transforming them with  
CC nucleic acid encoding CDK inhibitor or antisense construct complementary  
CC to the inhibitor gene, operably linked to a tissue-specific promoter.  
CC The transgenic plants exhibit alteration of traits such as petals, male  
CC sterility and ability to set seeds.

SQ Sequence 904 BP; 307 A; 107 C; 229 G; 261 T; 0 other;

Query Match 99.6%; Score 900.8; DB 21; Length 904;  
Best Local Similarity 99.8%; Pred. No. 3.2e-188;  
Matches 902; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atctctctctcaagagatgttaacttcacgcacacgtaacttaattcgaagatggtg 60  
DB 1 atctctctctccacagagatgttaacttcacgcacacgtaacttaattcgaagatggtg 60  
QY 61 aagaataatagaagaagcctaaaggaattgtaagaactggaatttcgtcaacgtatcgag 120  
DB 61 aagaataatagaagaagcctaaaggaattgtaagaactggaatttcgtcaacgtatcgag 120  
QY 121 ctacggagccggaggaattgtttatgtatagatcggaataaactcgtctcgcgtcgc 180  
DB 121 ctacggagccggaggaattgtttatgtatagatcggaataaactcgtctcgcgtcgc 180  
QY 181 ggtgtaatgaggttcgtctgtgtatgtagaagcaatgaattaaagaagaatta 240  
DB 181 ggtgtaatgaggttcgtctgtgtatgtagaagcaatgaattaaagaagaatta 240  
QY 241 ataatcttgagaggaagataaagatgtgacactgaacgttcgacgttcgacgggtg 300  
DB 241 ataatcttgagaggaagataaagatgtgacactgaacgttcgacgttcgacgggtg 300  
QY 301 acgagaggaagccttttgaataatctgagagaggaaggaagaagaattaaatc 360  
DB 301 acgagaggaagccttttgaataatctgagagaggaaggaagaagaattaaatc 360  
QY 361 atggaataattatcatcggaatttgaatcggcgggttaagaatcgttagattgttgt 420  
DB 361 atggaataattatcatcggaatttgaatcggcgggttaagaatcgttagattgttgt 420  
QY 421 agcggaggaagaaacgatgagagcgggtgaacggcgagggagggaggaagcgaattg 480  
DB 421 agcggaggaagaaacgatgagagcgggtgaacggcgagggagggaggaagcgaattg 480  
QY 481 atgacgagagatgccaaacggaatcgggaattttttgtggaagctgagaacaa 540

DB 481 atgacgagagatgccaaacggaatcgggaattttttgtggaagctgagaacaa 540  
QY 541 ctcaagaataattcaagaagaagtaacttcgatttcgagaagaagcattagaa 600  
DB 541 ctcaagaataattcaagaagaagtaacttcgatttcgagaagaagcattagaa 600  
QY 601 ggaacttgaacatgaggttaagttagagtgagaagaagaagaattatggtttttt 660  
DB 601 ggaacttgaacatgaggttaagttagagtgagaagaagaagaattatggtttttt 660  
QY 661 taacttttgaatttaataattcagggaataagtaatttttttttttttttttttt 720  
DB 661 taacttttgaatttaataattcagggaataagtaatttttttttttttttttttt 720  
QY 721 tataagatttgtagaggaatgtttttaagaatgacgaatttcacagaagaagaag 780  
DB 721 tataagatttgtagaggaatgtttttaagaatgacgaatttcacagaagaagaag 780  
QY 781 ctcttaacgattttagagccagaagaagtcgtgtcttttgcttacttaccctt 840  
DB 781 ctcttaacgattttagagccagaagaagtcgtgtcttttgcttacttaccctt 840  
QY 841 ctctgaatctgtgtatcttttagacatattctttagatattttatgttttggtagt 900  
DB 841 ctctgaatctgtgtatcttttagacatattctttagatattttatgttttggtagt 900  
QY 901 gata 904  
DB 901 gata 904  
RESULT 2  
ID AAC47352  
AAC47352 standard; DNA: 779 BP.  
AC AAC47352;  
DT 18-OCT-2000 (first entry)  
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 53499.  
DE  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway;  
KW metabolic pathway; promoter; termination sequence; ss.  
OS Arabidopsis thaliana.  
PX EPI033405-A2.  
PD 06-SEP-2000.  
PF 25-FEB-2000; 2000EP-0301439.  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123568.  
PR 23-MAR-1999; 99US-0125788.  
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PR 04-MAY-1999; 99US-0132407.  
PR 05-MAY-1999; 99US-0132484.  
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PR 04-OCT-1999; 99US-0157117.
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PR 29-OCT-1999; 99US-0162142.

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Query Match 85.7%; Score 774.8; DB 21; Length 779;

Best Local Similarity 99.7%; Pred. No. 1.3e-160; Indels 0; Gaps 0;

Matches 776; Conservative 0; Mismatches 2;

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QY 26 acttcacgcacacgtaacccaatacgaagaatggtgagaataatagaagaagcctaaagaa 85
DB 2 acttcacgcacacgtaacccaatacgaagaatggtgagaataatagaagaagcctaaagaa 61
QY 86 ttgtagaagcgtgaggttcgtcaacgcatatgcagctacggaacccggaagaattgtttatg 145
DB 62 ttgtagaagcgtgaggttcgtcaacgcatatgcagctacggaacccggaagaattgtttatg 121
QY 146 ttaagtcggaataatcaagctctgtcgcgtcgcgtcgtatgaatcgagcttcgctcctt 205
DB 122 ttaagtcggaataatcaagctctgtcgcgtcgcgtcgtatgaatcgagcttcgctcctt 181
QY 206 gtagtgagaagaatgaataatagaagaagaataataacatctcgggggaggaagaataag 265
DB 182 gtagtgagaagaatgaataatagaagaagaataataacatctcgggggaggaagaataag 241
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DB 242 atggtgacacgcgaacgctcgcgcgtatgcagcgggtgacgaagaagaagccttttgaataac 301
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RESULT 3
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ID AAC36958 standard; DNA; 780 BP.
XX
AC AAC36958;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 15673.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 08-APR-1999; 99US-0128714.
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PR 01-JUN-1999; 99US-0137222.
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PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.

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XX 07-APR-1999; 99US-0128192.
PR (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Klein TM, Weng Z, Cahoon RE;
XX MPI: 2000-679375/66.
XX P-PSDB: AAP01953.
DR
XX
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
PT herbicides and plant growth inhibitors
XX
XX Claim 2; Page 51; 58pp; English.
XX
XX The invention describes a novel isolated polynucleotide comprising a
CC nucleotide sequence encoding one of 17 specific cyclin dependent kinase
CC inhibitor (CDKI) polypeptides, cell cycle regulators involved in
CC control of cell division, growth and death. The nucleotide sequences can
CC be used in a vector to transform a host cell to produce the CDKI
CC polypeptide. They can also be used in methods for selecting and
CC obtaining a nucleic acid sequence that encodes CDKI or affects the level
CC of CDKI expression. The encoded protein can be used in a method for
CC evaluating a compound for its ability to inhibit the activity of a CDKI.
CC The inhibitors can be used as herbicides. They can also be used to
CC inhibit plant growth. The polynucleotide sequences can be used in gene
CC mapping and as genetic markers. The sequence encodes the soybean CDKI
CC clone s12.pK0117.h4 as described in the method of the invention.
XX
SQ Sequence 470 BP; 155 A; 73 C; 91 G; 151 T; 0 other;

Query Match 7.9%; Score 71.6; DB 21; Length 470;
Best Local Similarity 67.3%; Pred. No. 1.6e-06;
Matches 101; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 491 tgcacaggaatcgaagaattggaattttgtggaagctgagaagaactcaagaagaa 550
D 42 tcccaacgagtcgagagctcgaagattcttcgtcgtcgagagaacacattcagaagaa 101
QY 551 aattcaagaagaagtaacattcgattcgagaagaagagccattagaagagcttaag 610
D 102 gctccacagacagataattatgattttgtgaagagacatgcttggagagacataag 161
QY 611 aatgggtaagttagatgagtaagaagaagaa 640
D 162 agtgggttaattgaagtcataaagaatgaa 191

RESULT 6
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ID AAA95289 standard; cDNA; 470 BP.
XX
XX AAA95289;
XX
XX 17-JAN-2001 (first entry)
XX
XX Soybean cyclin-dependent kinase inhibitor coding sequence #4.
XX
XX Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
XX CKI; cell growth; herbicide; ss.
XX
XX Glycine max.
XX
XX OS
XX FH Key Location/Qualifiers
XX CDS 2..184
XX FT /tag= "CDKI"
XX FT /product= "CDKI"
XX FT /partial
XX
XX MO200060087-A2.
XX
XX 12-OCT-2000.

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XX 06-APR-2000; 2000WO-US09106.
PR
XX 07-APR-1999; 99US-0128192.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX Klein TM, Weng Z, Cahoon RE;
XX MPI: 2000-679375/66.
XX P-PSDB: AAB27255.
DR
XX
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
PT herbicides and plant growth inhibitors
XX
XX Claim 2; Page 51; 58pp; English.
XX
XX The present sequence is the coding sequence for the soybean
CC cyclin-dependent kinase inhibitor (CDKI). It was isolated by searching a
CC soybean seedling cDNA library for sequences similar to those encoding the
CC CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis
CC thaliana. CDKI is involved in the cell cycle, and may promote or inhibit
CC cell division and growth. The coding sequence and the protein it encodes
CC are useful in the production of transgenic plants which produce increased
CC or decreased amounts of the CDKI protein, in the identification of the
CC herbicides, in genetic and physical mapping and in the isolation of the
CC CDKI gene in other organisms.
XX
SQ Sequence 470 BP; 155 A; 73 C; 91 G; 151 T; 0 other;

Query Match 7.9%; Score 71.6; DB 21; Length 470;
Best Local Similarity 67.3%; Pred. No. 1.6e-06;
Matches 101; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 491 tgcacaggaatcgaagaattggaattttgtggaagctgagaagaactcaagaagaa 550
D 42 tcccaacgagtcgagagctcgaagattcttcgtcgtcgagagaacacattcagaagaa 101
QY 551 aattcaagaagaagtaacattcgattcgagaagaagagccattagaagagcttaag 610
D 102 gctccacagacagataattatgattttgtgaagagacatgcttggagagacataag 161
QY 611 aatgggtaagttagatgagtaagaagaagaa 640
D 162 agtgggttaattgaagtcataaagaatgaa 191

RESULT 7
AAC33295
ID AAC33295 standard; DNA; 1341 BP.
XX
XX AAC33295;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 2504.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX OS
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.

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PR 23-MAR-1999; 99US-0125788.  
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PR 06-OCT-1999; 99US-0157865.

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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161921.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 7.1%; Score 63.8; DB 21; Length 1341;
Best Local Similarity 61.7%; Pred. No. 0.00011;
Matches 119; Conservative 0; Mismatches 72; Indels 2; Gaps 1;

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QY 493 ccaacggaatcggaattgaatttttttgggaagctggaacacaaagaagaa 552
DB 377 ccaacacaccgcgaatggaagatttctcggggtcgtggaagaacacagaagaa 436
QY 553 ttcagaagaagatcacatttcgatttcgagaagaagcattagaagagcgttacgaa 612
DB 437 ttcattggaagaagtaacatttgatcctgtggaacgaacacacacagcggtttgaa 496
QY 613 tgggttaagttaga--gttaagaagaagaagatttattgttttttttaactttta 670
DB 497 tggacgaagtgatgatttagaacaacaaaaaatgggggttaattatgtaatacagaa 556
QY 671 gatttaataatt 683
DB 557 tatattaacattt 569

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RESULT 8
ID AAN02401 standard; DNA: 620 BP.
XX AAN02401:
AC
XX
DT 01-NOV-2001 (first entry)
XX
DE Cyclin dependent kinase inhibitor (CDKI) clone s12.pK0008.d2:fls.
XX
KW Cyclin dependent kinase inhibitor; CDKI; herbicide; cell cycle;
XX soybean; plant growth inhibitor; ds.
OS Glycine max.
XX
XX Key Location/Qualifiers
XX Key 1..264
XX CDS /*tag- a
FT /product- "CDKI fragment"
FT /partial

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FT /note= "No start codon given"
XX
XX WO2000060957-A2.
XX
XX 12-Oct-2000.
XX
XX 06-APR-2000; 2000WO-US09106.
XX
XX 07-APR-1999; 99US-0128192.
XX
XX (DDBP) DU POINT DE NEMOURS & CO E.I.
XX
XX Klein TM, Weng Z, Cahoon RE.
XX
XX WPI: 2000-679375/66.
XX
XX P-PSDB; AAP01951.
XX
XX Cyclin dependent kinase inhibitor sequences, useful for identifying
XX herbicides and plant growth inhibitors
XX
XX Claim 2: Page 49; 58pp; English.
XX
XX The invention describes a novel isolated polynucleotide comprising a
XX nucleotide sequence encoding one of 17 specific cyclin dependent kinase
XX inhibitor (CDKI) polypeptides, cell cycle regulators involved in
XX control of cell division, growth and death. The nucleotide sequences can
XX be used in a vector to transform a host cell to produce the CDKI
XX polypeptide. They can also be used in methods for selecting and
XX obtaining a nucleic acid sequence that encodes CDKI or affects the level
XX of CDKI expression. The encoded protein can be used in a method for
XX evaluating a compound for its ability to inhibit the activity of a CDKI.
XX The inhibitors can be used as herbicides. They can also be used to
XX inhibit plant growth. The polynucleotide sequences can be used in gene
XX mapping and as genetic markers. The sequence encodes the soybean CDKI
XX clone s12.pK0008.d2:fls as described in the method of the invention.
XX
XX Sequence 620 BP; 191 A; 111 C; 134 G; 183 T; 1 other:

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Query Match 7.0%; Score 63; DB 21; Length 620;
Best Local Similarity 64.1%; Pred. No. 0.00014;
Matches 93; Conservative 1; Mismatches 51; Indels 0; Gaps 0;
QY 490 atgcacgaagaaatgaattgaatttttttgggaagctggaacacaaagaagaa 549
DB 121 atgcaccgagttggagctcggaatttctcgttgcgtgggaagagacattcagaa 180
QY 550 aaattcaagaagaatcacatttcgatttcgagaagaagcattagaagaagcgttac 609
DB 181 cgatttcaagaagaatcacatttattgttgaagagcgtacacactggaagcgtctac 240
QY 610 gaatgggttaagttagatgaaagaa 634
DB 241 gagggggttcagttgaagccatgaa 265

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RESULT 9
ID AAA95287 standard; CDNA: 620 BP.
XX AAA95287:
AC
XX
DT 17-JAN-2001 (first entry)
XX
DE Soybean cyclin-dependent kinase inhibitor coding sequence #2.
XX
KW Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division;
XX CDKI; cell growth; herbicide; ss.
OS Glycine max.
XX
XX Key Location/Qualifiers
XX Key 1..264
XX CDS

```



XX antiarteriosclerotic; antianemic; cytosstatic; nootropic;  
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KW antineumatic; antiarthritic; antidiabetic; antipsoriatic;  
 KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
 KW gene; ds.  
 XX Homo sapiens.  
 XX NO200200928-A2.  
 XX 03-JAN-2002.  
 XX 02-JUL-2001; 2001MO-EP07537.  
 XX 30-JUN-2000; 2000DE-1032529.  
 XX 01-SEP-2000; 2000DE-1043826.  
 XX (EPiG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI: 2002-130909/17.  
 XX Nucleic acid comprising fragment of chemically modified gene, useful  
 PT for diagnosis and treatment of diseases associated with abnormal  
 PT cytosine methylation -  
 PS Claim 1; SEQ ID NO 1294; 32pp + Sequence Listing; German.  
 XX The present invention provides a number of human immune system associated  
 CC genes which are modified by the methylation of cytosines. The sequences  
 CC can be used in the diagnosis and treatment of immune system disorders,  
 CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention.  
 XX SQ Sequence 16509 BP; 4031 A; 379 C; 3836 G; 8263 T; 0 other;

Query Match 6.7%; Score 60.6; DB 24; Length 16509;  
 Best Local Similarity 54.8%; Pred. No. 0.0012;  
 Matches 120; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 665 aggaataagtaatttcttctgttgaattggaatataagattgtaggaagtgtt 744  
 Db 15468 aggggttaattttttattttatttagattgagaattgaggttttataaggagaagtcg 15547  
 QY 745 tttaagaagtaacatgcacagaagaagaagcttttaacagatttagagccca 804  
 Db 15548 atctgttttagttcataaggggtacagagagtgatggaattgggtttattttata 15607  
 QY 805 gaaaagtcgtctttagctctaccttcttacccttccttcgaactcgtgtacctttag 864  
 Db 15608 ttgaatttttttttttaattgctgtttaaattgttttaacttagcgtttattcttg 15667  
 QY 865 catattcttagtaacattttattgtttgttgactgat 903  
 Db 15668 tttatttttagttaatttaagttttagttgtagt 15706

RESULT 12  
 AAA95293  
 ID AAA95293 standard; CDNA; 870 BP.  
 XX  
 AC AAA95293;  
 XX  
 DT 17-JAN-2001 (first entry)  
 XX  
 DE Arabidopsis thaliana cyclin-dependent kinase inhibitor coding sequence.

XX Cyclin-dependent kinase inhibitor; cell cycle; cell division;  
 KW CDKI; cell growth; herbicide; ss.  
 KW Arabidopsis thaliana.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..870  
 FT CDS /\*tag= a  
 FT /product= "CDKI"  
 XX  
 XX NO200060087-A2.  
 XX 12-OCT-2000.  
 XX 06-APR-2000; 2000MO-US09106.  
 XX 07-APR-1999; 99US-0128192.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E. I.  
 XX Klein TM, Weng Z, Cahoon RE;  
 XX WPI: 2000-679375/66.  
 XX P-PSDB: AAB27262.  
 XX Cyclin dependent kinase inhibitor sequences, useful for identifying  
 PT herbicides and plant growth inhibitors -  
 PS Disclosure; Page 56-57; 58pp; English.  
 XX The present sequence is the coding sequence for the Arabidopsis thaliana  
 CC cyclin-dependent kinase inhibitor (CDKI). It was used in the isolation of  
 CC sequences from wheat, corn, rice and soybean encoding the CDKI protein.  
 CC CDKI is involved in the cell cycle, and may promote or inhibit cell  
 CC division and growth. The coding sequence and the protein it encodes are  
 CC useful in the production of transgenic plants which produce increased or  
 CC decreased amounts of the CDKI protein, in the identification of  
 CC herbicides, in genetic and physical mapping and in the isolation of the  
 CC CDKI gene in other organisms.  
 XX SQ Sequence 870 BP; 265 A; 185 C; 203 G; 217 T; 0 other;

Query Match 6.7%; Score 60.4; DB 21; Length 870;  
 Best Local Similarity 65.7%; Pred. No. 0.00056;  
 Matches 88; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 493 ccaacgagatcggaattgaagtgttttctgtgaagctgagaaacactcaagaagaaa 552  
 Db 730 ccaactaacctgaattggaagattttcttcggtgctgaaagaacaacagaagcaaa 789  
 QY 553 ttcaagaagaatgaatttcgatttcgaagaaggaagcatttagaagagttacgaa 612  
 Db 790 ttcatgtggaagtagcaactttgtatcctgtgaacgaacacactaccagagcgtttgaa 849  
 QY 613 tgggttaagttaga 626  
 Db 850 tggacgaaggtaga 863

RESULT 13  
 AAC46465  
 ID AAC46465 standard; DNA; 870 BP.  
 XX  
 AC AAC46465;  
 XX  
 DT 18-OCT-2000 (first entry)  
 XX  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 50239.  
 XX  
 KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway;

metabolic pathway; promoter; termination sequence; ss.  
Arabidopsis thaliana.  
EP1033405-A2.  
06-SEP-2000.  
25-FEB-2000; 2000EP-0301439.  
99US-0121825.  
99US-0123180.  
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13-AUG-1999; 99US-0148565.  
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20-AUG-1999; 99US-0149722.  
20-AUG-1999; 99US-0149929.  
23-AUG-1999; 99US-0149902.  
23-AUG-1999; 99US-0149930.  
25-AUG-1999; 99US-0150560.  
26-AUG-1999; 99US-0150884.  
27-AUG-1999; 99US-0150884.  
27-AUG-1999; 99US-0151066.  
27-AUG-1999; 99US-0151067.  
30-AUG-1999; 99US-0151303.  
31-AUG-1999; 99US-0151438.  
01-SEP-1999; 99US-0151930.  
07-SEP-1999; 99US-0152363.

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PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154038.
PR 20-SEP-1999; 99US-0154772.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159684.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160814.
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PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
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PR 29-OCT-1999; 99US-0162142.

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DB 730 ccaactacacctgaatgagcgagttttctcgcgtcgaagaagaacaacagaagcaa 789
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QY 613 tgggtaaagttaga 626
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RESULT 14
AAK25038
ID AAK25038 standard; DNA: 69 BP.
XX
AC AAK25038;
XX
DT 05-JUL-1999 (first entry)
XX
DE Cyclin-dependent kinase inhibitor LDV159 cDNA PCR primer.
XX
KW Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI;

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KW LDV159; CKI; plant development; transgenic plant; cell cycle;
KW growth regulator; herbicide; PCR; primer; ss.
XX
OS Synthetic.
OS Arabidopsis thaliana.
PN WO9914331-A2.
XX
PD 25-MAR-1999.
PF 16-SEP-1998; 98MO-EP05895.
PR 24-DEC-1997; 97EP-0204111.
PR 16-SEP-1997; 97EP-0202838.
XX
PA (CROP-) CROPPDESIGN NV.
PI De Almeida J, De Veylder L, Inze D, Landrieu I;
XX WPI; 1999-229535/19.
DR
XX DNA encoding inhibitor of cyclin-dependent kinase
XX
PS Example 10; Page 56; 88pp; English.
XX
CC The present sequence was used as a primer, together with the primer
CC given in AAK25039, for the PCR amplification of LDV159 cDNA coding
CC region. LDV159 is a cyclin-dependent kinase (CDK) inhibitor of
CC Arabidopsis thaliana, and is identical to previously known CKI.
CC The PCR fragment was cloned into vector pTA7002. The resulting
CC binary vector was transferred into Agrobacterium tumefaciens and
CC used to transform tobacco cv. Petit Havana to produce transgenic
CC plants that overexpressed the CDK inhibitor. Several CDK
CC inhibitors have been shown to exist in plants. They are expressed
CC at different time points and may have different functions during
CC the development of the plant. CDK inhibitors, nucleic acids,
CC antibodies, promoter sequences, related recombinant DNA and
CC vectors are all useful for: modulating the cycle, division and/or
CC growth of plant cells; altering activity of CDK; modulating growth
CC inhibition in plants caused by environmental stress; inducing male
CC or female sterility; altering cell division progression in plants,
CC bacteria, fungi, insect and animal cells; and screening for
CC agonists or antagonists that are potentially useful as growth
CC regulators or herbicides.
XX
SQ Sequence 69 BP; 24 A; 10 C; 19 G; 16 T; 0 other;

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Query Match 6.6%; Score 59.4; DB 20; Length 69;
Best Local Similarity 98.4%; Pred. No. 0.00045;
Matches 60; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 53 agatggtgaaataatagaaagctaaaggaattagaagctgagatttcgtaacgt 112
    ||||| | | ||||| | | ||||| | | ||||| | | ||||| | | ||
DB 9 agatggtgaaataatagaaagctaaaggaatttcgtaagctgagatttcgtaacgt 68
QY 113 a 113
DB 69 a 69

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RESULT 15
ABL33226
ID ABL33226 standard; DNA: 13125 BP.
XX
AC ABL33226;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 1199.
XX
KW Human; immune system disease; cytosine methylation; antistimatic;
antiartherosclerotic; antiinflammatory; cyostatic; nootropic;

```

KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KM	antiheumatic; antirheumatic; antidiabetic; antipsoriatic;
KV	antihypertensive; cancer; eye disease; arteriosclerosis; anaemia;
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KM	neutrophilic dermatitis; rheumatoid arthritis; psoriasis; bowel disease;
KW	gene; ds.
XX	
OS	Homo sapiens.
XN	
PN	N0200200928-A2.
PD	
XX	
PD	03-JAN-2002.
XX	
PF	02-JUL-2001; 2001WO-EP07537.
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
P1	Olek A., Piepenbrock C., Berlin K.;
DR	WPI; 2002-130909/17.
XX	
PT	- Nucleic acid comprising fragment of chemically modified gene, useful
PT	for diagnosis and treatment of diseases associated with abnormal
PT	cytosine methylation -
XX	
PS	Claim 1; SEQ ID NO 1199; 32bp + Sequence Listing; German.
XX	
CC	The present invention provides a number of human immune system associated
CC	genes which are modified by the methylation of cytosines. The sequences
CC	can be used in the diagnosis and treatment of immune system disorders,
CC	including eye diseases such as retinopathy, neovascular glaucoma and
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC	leukemia, Alzheimer's disease, AIDS, epilepsy, neutrophilic dermatitis,
CC	rheumatoid arthritis, psoriasis and inflammatory/allergative bowel
CC	diseases. The present sequence is a gene of the invention.
XX	
SQ	Sequence 13125 BP; 3546 A; 246 C; 2776 G; 6555 T; 2 other;
	Query Match            6.5%; Score 58.8; DB 24; Length 13125;
	Best Local Similarity   53.8%; Pred. No. 0.0027;
	Matches 143; Conservative   0; Mismatches 122; Indels   1; Gaps   1
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QY	696 taattatttttgttgaattggaaataagaattgttagaggaagtgttttagaagtac 755
DB	7475 tagatttgttttttttgtattattttttaaaaactcggttgaagtattatatagag 7534
QY	756 gaattgcacagaaaaagaagaaccttttaacgatttttagagccagaaaag-tcgt 814
DB	7535 gaaagggtataataataagaatgtagatttaacgaatttttaaaaacgatacgtttg 7594
QY	815 gtcttttagcctacttttacccttccttcgaaatcttgytatcttttagaatacttc 874
DB	7595 gtatttttagattaagaataagataattatgtgaatttttagaagtttttttggtttttt 7654
QY	875 agtaaattttaagttttttggtgact 900
DB	7655 gtaataagataatcagttttttgatt 7680

GenCore Version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 15:54:59 ; Search time 1823.05 seconds  
(without alignments)  
10376.890 Million cell updates/sec

Title: US-09-733-507-1

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Scoring table: IDENTITY\_NUC  
Gapex 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_hg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_to:\*
- 11: gb\_sy:\*
- 12: gb\_un:\*
- 13: gb\_vi:\*
- 14: gb\_vl:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
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- 25: em\_pl:\*
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- 28: em\_vi:\*
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- 30: em\_hg\_hum:\*
- 31: em\_hg\_inv:\*
- 32: em\_hg\_inv:\*
- 33: em\_hg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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1	904	100.0	904	6	AX008791	AX008791 Sequence
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3	656.8	72.7	660	6	AX008793	AX008793 Sequence
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5	543.2	60.1	98374	8	AC003040	AC003040 Arabidops
6	364	40.3	443	6	AX008794	AX008794 Sequence
7	339.2	37.5	377	6	AX008795	AX008795 Sequence
8	92.6	10.2	7218	6	AB02943	AB02943 Sequence 14
9	75	8.3	927	8	AB029433	AB029433 Pisum sat
10	72.4	8.0	804	6	AX008805	AX008805 Sequence
11	72.4	8.0	804	8	CRJ002173	AX002173 Chenopodi
12	69.4	7.7	789	8	NT0297306	NT0297306 Nicotiana
13	69	7.6	286564	2	AC091428	AC091428 Mus muscu
14	66.8	7.4	203606	2	AL645990	AL645990 Mus muscu
15	65	7.2	223547	2	AL611963	AL611963 Mus muscu
16	64.6	7.1	223828	2	AC098731	AC098731 Mus muscu
17	64.2	7.1	231122	2	AC090480	AC090480 Mus muscu
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19	62.8	6.9	282611	2	AL645746	AL645746 Mus muscu
20	62.6	6.9	161475	9	HS164C20	AL009039 Homo sapi
21	62.2	6.9	203984	2	AC067854	AC067854 Homo sapi
22	62	6.9	111345	2	AL445531	AL445531 Human DNA
23	62	6.9	236962	2	AL606742	AL606742 Mus muscu
24	61.8	6.8	157848	9	AC079763	AC079763 Homo sapi
25	61.6	6.8	63739	2	AC102458	AC102458 Mus muscu
26	61.6	6.8	75241	2	AC102370	AC102370 Mus muscu
27	61.6	6.8	179149	9	AC009785	AC009785 Homo sapi
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29	61.6	6.8	252957	2	AC0105705	AC105705 Rattus no
30	61.4	6.8	153588	9	AC010533	AC010533 Homo sapi
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## ALIGNMENTS

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1	AX008791	Sequence 1 from Patent WO9964599.	904 bp	DNA	linear	PAT 06-SEP-2000							
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 904)  
Fowke, L.C., Wang, H. and Crosby, W.L.  
Cyclic-dependent kinase inhibitors as plant growth regulators  
Patent: WO 9964599-A 1 16-DEC-1999;  
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD  
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILIAM L (CA); UNIV  
SASKATCHEWAN TECHNOLOGIES (CA)

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source location/Qualifiers  
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ACCESSION AX008793  
VERSION AX008793.1 GI:9996257  
KEYWORDS  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 660)  
REFERENCE Fowke, L.C., Wang, H., and Crosby, W.L.  
AUTHORS Cyclin-dependent kinase inhibitors as plant growth regulators  
TITLE Patent: WO 9964599-A 3 16-DEC-1999;  
JOURNAL FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD  
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV  
SASKATCHEWAN TECHNOLOGIES (CA)  
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Location/Qualifiers  
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BASE COUNT 232 a 66 c 186 g 176 t  
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Query Match 72.7%; Score 656.8; DB 6; Length 660;

Best Local Similarity 99.7%; Pred. No. 4.9e-121;  
Matches 658; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 109 acgtatgacagctacgagccggaagaattgttaatttagatcggaaaaatcaagctct 168  
| | | | |  
Db 1 ACGTATGACAGCTACGAGCCCGAGAAATGTTATGTTATGATCGGAAATCAACTCT 60  
QY 169 gtctccctcgtcgtgataatggaatttcgtctgtgtatgttgaagaatgataaag 228  
| | | | |  
Db 61 GTCTCGTGTGCTGGGATATGAGATTTTCTGCTCTTCTGTAGACCAATGAAATTAAG 120  
QY 229 aagaaagaattatacatctggaagaggaataaagatggttacactgaacgttcgag 288  
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Db 121 AAGAAAGATTAATATCATCTGAGAGAGAAATTAATGATGCTGACATGAAAGTGCAG 180  
QY 289 tatcgacgggtgagcaagaagaacatttgaataatcgaagaagaaggaagaaga 348  
| | | | |  
Db 181 TATCAGCGGGGTACGAAAGAGAGCTTTTGAATCTGAGAGAGAGAGAGAGAGAA 240  
QY 349 ttaagtaaatccatgagaaattatcatcgcgaatttgaatcgagcggttaagaatcgtta 408  
| | | | |  
Db 241 TTAAGTAAATCCATGAGAAATTTATTCATCGGAATTTGAATGGCGGTTAAAGAAATCGTTA 300  
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Db 301 GATTGTTGTTGAGCGGAGGAGAAACGATGAGAGAGAGGTGACGCGGAGAGAGAGAG 360  
QY 469 aagggcaaatgatgacgagagatgcgaacggaatcggaatcttctgtgaa 528  
| | | | |  
Db 361 AAGCGGAATTTGATACGAGATGCCAGAGAGAGAAATGGAATTTTGTGCGAA 420  
QY 529 gctgagaaacaaactaaagaagaatcaagaagaatcaaatctgcgaatcgagaagag 588  
| | | | |  
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AF079587 1240 bp DNA linear PLN 07-SEP-1998  
LOCUS AF079587  
DEFINITION Arabidopsis thaliana cyclin-dependent kinase inhibitor (ICK1) gene,  
complete cds.  
ACCESSION AF079587  
VERSION AF079587.1 GI:3550261  
KEYWORDS  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 1240)  
REFERENCE Wang, H., Qi, Q., Schorr, P., Cutler, A.J., Crosby, W.L. and Fowke, L.C.  
AUTHORS ICK1, a cyclin-dependent protein kinase inhibitor from Arabidopsis  
TITLE thaliana interacts with both Cdc2a and Cdc2b, and its expression is  
induced by abscisic acid  
JOURNAL Plant J. 15 (4), 501-510 (1998)  
MEDLINE 98426383  
REFERENCE 2 (bases 1 to 1240)  
AUTHORS Wang, H.  
TITLE Direct Submission  
JOURNAL Submitted (21-JUL-1998) Saskatoon Research Centre, Agriculture and  
Agri-Food Canada, 107 Science Place, Saskatoon, SK S7N 0X2, Canada





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/notes="hypothetical protein"
/codon.start=1
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/db_xref="GI:3242703"
/translation="MMTRNGSLRFPNMTFSYDEATCVREELIQRELMFRHVSFIL
DGNRRRAKRGDLTQAQHEAGTKRIEIAERIGETREVRVSIGNTKIPELSLKE
IHEIEBATKATRISISSWQ"
Query Match      60.1%; Score 543.2; DB 8; Length 98374;
Best Local Similarity 73.3%; Pred. No.2,1e-98;
Matches 901; Conservative 0; Mismatches 3; Indels 326; Gaps 3;
QY 1 attctctctctcacagagattgtaacttaacgacacgtaacctaataatcgaaatggtg 60
Db 29340 ATCTCTCTCTCACAGAGATTGTAAGCTTACGACACAGTAACCTAAACGAAGATGGAG 29281
QY 61 agaaataaagaaagcgaagaaatgtagaagctggaatttcgtaacgataatcgacg 120
Db 29280 AGAAATATTAAGAAAGCTAAAGCAATGTGAAAGCTGAGATTTCGTAACGATTAACGAG 29221
QY 121 ctacgagccgagagaattgttataatgtagatcggaataacaaagctctgtccgcgtgc 180
Db 29220 CTACGAGCCGAGAGATTGTTATGTTAGATCGGAAAAACAAGCTGTCTCCGTCGTC 29161
QY 181 ggtgtaatggaattgctgctctgtagtgaagcaataataagaagaagatta 240
Db 29160 GGTGTAATGAGAGTTGCTGCTCTGTAGTGAAGCATATAAGAAAGAAATTA 29101
QY 241 atacatctcg----- 250
Db 29100 ATACATCTGAGAGTTATTTAATGTTGATTCTAGATCTGTGAACCTGATATGATCA 29041
QY 251 ----- agagaggaagtaaat 267
Db 29040 TTTAATGTTAATGTAATTTTTTTTTTGAATTTTGAATTTTGTAGGAGAAATTAAGAT 28981
QY 268 ggtgacactgaacgctacgac----- 295
Db 28980 GGTGACACTGAAAGCTGACGTATCGACGCGTAGCTGTTAAAAAAAACGAAATGATT 28921
QY 296 ----- 295
Db 28920 TGAATTTTGAAGTTTATTTATTTCCCGGTTATTTTGAAGTCTCTCTCAATAAATT 28861
QY 296 -----99gtacgaagaaggaagctttttaaacttgag 329
Db 28860 TAGAATCTTGTGCTTGAGATTATTTAGGGGTACGACAGAGAGAGTTTAAAAATCGAG 28801
QY 330 agagagagagaaagaagaattcaagtaaatcctgagaaatattcatcggaatttgaatc 389
Db 28800 AGAGAGAGGAGAAAGAGATTAAATTCATGAGAAATTTATTCATCGGAATTTGAATC 28741
QY 390 ggcgggttaagaatcgttagaattgttgttagcggagagaaacgaatgagagagaggt 449
Db 28740 GGCGGTTAAGAAATCGTAGATTGTGTGTAGCGGAGGAGAAACGATGAGAGACGGT 28681
QY 450 gacggcgagagagagagaggaagcgaaatgtagcaggaatgccaacggaatcggaat 509

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Db 28680 GAGCGCCGAGAGAGAGAGAGCGCAATTTGATGACGAGAGCCAGGATCGGAAT 28621
QY 510 tgaagatttttggtagaactgagaaacactcaagaagaattcaagaaga----- 563
Db 28620 TGAAGATTTTGTGGAAGCTGAGAAACACTCAAGAAAAATTCAGAGAAAGTAAGT 28561
QY 564 ----- 563
Db 28560 TTTATTTTATTTGTGAGTTGATTTTATAGATATATATTTTATTCATAATTTAA 28501
QY 564 ----- gtaacattcg 574
Db 28500 AATTGATTTGAGGTAAATTAAGATGAGTTATTTTATTTTATTTAGTTCATTTG 28441
QY 575 attcsgaagaggaagccatlagagaagacgttacgaatcggttaagtagagtagaagaa 634
Db 28440 ATTTCGAGAGGAGAAACCATTTAGAGAGAGCTTACCAATGGTAAAGTTAGAGTAAGAA 28381
QY 635 gaagaagaagttatggttttttttaacttttagatatttaataatcagggagataag 694
Db 28380 GAAAGAAAGCTTATAGTTTTTTTTTTTAACTTTTATGATTTAATTTTCAAGGAATAG 28321
QY 695 ttaattattttgttgatttggaataataagaattgtagaggaatgltttagaagta 754
Db 28320 TTAATTTATTTTGTGATTTGGAATATATAGATTTTGAGAGGAATGTTTAAAGTA 28261
QY 755 cgaattgcacagaagaagaagaagcttttaacagattttagagccagagaagatgct 814
Db 28260 CGAAATGCAACAGAAAGAGAAAGCTTTTAAACAGATTTTAAAGACCAGAAAGTGCT 28201
QY 815 gttcttagctctacttaccctctcttcgaactctgtatccttttagatattcctt 874
Db 28200 GTCTTTAGCTCTACTTTTACCTCTCTTGATCTTGATCTGTGATCTTTTGAATATCTTT 28141
QY 875 agtacattttatggttttggtagatgata 904
Db 28140 AGTACATTTTATGTTTTTTGTGATGATGATA 28111

RESULT 6
AX008794 AX008794 443 bp DNA linear PAT 06-SEP-2000
LOCUS AX008794 Sequence 4 from Patent WO964559.
DEFINITION AX008794
VERSION AX008794.1 GI:9996258
KEYWORDS
SOURCE
thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 443)
AUTHORS Fowke,L.C., Wang,H. and Crosby,W.L.
TITLE Cyclin-dependent kinase inhibitors as plant growth regulators
JOURNAL Patent: WO 9964599-A 4 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
FEATURES
source 1..443
/organism="Arabidopsis thaliana"
BASE COUNT 149 a 45 c 123 g 126 t
ORIGIN
Query Match 40.3%; Score 364; DB 6; Length 443;
Best Local Similarity 100.0%; Pred. No.9.7e-63;
Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 361 atggaagaatttcacatcgaaattgaatcgcggttaagaagaatcgtaattgtgtct 420
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Db 80 ATGAGAAATATTCATCGGAATTTGAAATCGGGTAAAGATCGTTAGATTGTTGT 139  
QY 421 agcgagggaacacatgagagacggtgagacgagagagagagagagagagag 480  
Db 140 AGCGGAGAGAAACGATGAGAGACGCGTGAAGCGGAGAGAGAGAGAGAGAG 199  
QY 481 atgacgagatgccaacggaatcggaattgagaatttttctgtgaaagctgaga 540  
Db 200 ATGACGGAATGCGACGGAATCGGAATTTGGAATTTTTCGAGAGAGAGAGAG 259  
QY 541 ctcaagaaaattcaagagaatgacaatttcgatttcgagagagagagagagag 600  
Db 260 CTCGAAAGAAATTCAGAGAGAGATTCGATTTCGAGAGAGAGAGAGAGAGAG 319  
QY 601 ggaactacgaatgagtaagtaagtaagtaagtaagtaagtaagtaagtaag 660  
Db 320 GACGCTTACGAATGGCTAAAGTTAGTGAAGAGAGAGAGAGAGAGAGAGAG 379  
QY 661 taacttttagatttaataatttcgaggaataagtaatttatttttctgattg 720  
Db 380 TAACCTTTTGAATTTTAAATTTTCAAGGAGATTAATTTTATTTGTTGTTG 439  
QY 721 tata 724  
Db 440 TATA 443

RESULT 7  
AX008795 377 bp DNA linear PAT 06-SEP-2000  
LOCUS Sequence 5 from Patent WO9964599.  
DEFINITION AX008795  
ACCESSION AX008795  
VERSION AX008795.1 GI:9996259  
KEYWORDS  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
1 (bases 1 to 377)  
REFERENCE  
AUTHORS Fowke, L.C., Wang, H. and Crosby, W.L.  
TITLE Cyclin-dependent kinase inhibitors as plant growth regulators  
JOURNAL Patent: WO 964599-A 5 16-DEC-1999;  
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD  
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV  
SASKATCHEWAN TECHNOLOGIES (CA)  
FEATURES  
Source Location/Qualifiers  
1..377  
/organism="Arabidopsis thaliana"  
/db\_xref="taxon:3702"  
BASE COUNT 138 a 31 c 109 g 99 t  
ORIGIN

Query Match 37.5%; Score 339.2; DB 6; Length 377;  
Best Local Similarity 94.1%; Pred. No. 8; 4e-58;  
Matches 369; Conservative 0; Mismatches 8; Indels 15; Gaps 1;

QY 285 gacatcgcagcgtgagcgaagagagagagagagagagagagagagagagag 344  
Db 1 GAGTATTTTAAAGGGGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60  
QY 345 agaattagaatcaatcagagagagagagagagagagagagagagagagagag 404  
Db 61 AGAATTAAGTAAATCCATGAGAGATTAATCATGGAATTTGAATCGCGTTAAAGAAC 120  
QY 405 gttagattgtgtgtgtagcgagagagagagagagagagagagagagagagag 464  
Db 121 GTTAGATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 165  
QY 465 ggaag 524  
Db 166 GGAGAGGCGAAATTTGATGACGAGATGCCAACGAGATCGGAATTTGAAATTTTGT 225

QY 525 ggaagctgagaaacaactcaagaaataatcaagaaagagagagagagagag 584  
Db 226 GGAAGCTGAGAAACACCTCAAGAAATTCAGAGAGAGATGATTTGATTTGAGAA 285  
QY 585 ggaagagccattagaagagagagagagagagagagagagagagagagag 644  
Db 286 GGAGAGCCATTAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 345  
QY 645 tttaggttt 676  
Db 346 TTTAGCTTTTtt 377  
RESULT 8  
166494/c 7218 bp DNA linear PAT 28-DEC-1997  
LOCUS 166494 Sequence 14 from patent US 5670367.  
DEFINITION 166494  
ACCESSION 166494  
VERSION 166494.1 GI:2724471  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 7218)  
AUTHORS Dörner, F., Schefflinger, F. and Falkner, F. Gunter.  
TITLE Recombinant fowlpox virus  
JOURNAL Patent: US 5670367-A 14 23-SEP-1997;  
DEFINITION Location/Qualifiers  
FEATURES  
Source 1..7218  
/organism="unknown"  
BASE COUNT 1944 a 1491 c 1486 g 1929 t 368 others  
ORIGIN

Query Match 10.2%; Score 92.6; DB 6; Length 7218;  
Best Local Similarity 4.9%; Pred. No. 1; 1e-08;  
Matches 20; Conservative 255; Mismatches 134; Indels 0; Gaps 0;

QY 237 attaatcctcgtgagagagagagagagagagagagagagagagagagagag 296  
Db 1473 ATCTATGCAAGTATGTTAAAGAGATGAGAAATTTGCTCRRRRRRRRRRRRRR 1414  
QY 297 ggtcagcag 356  
Db 1413 RRR 1354  
QY 357 atccag 416  
Db 1353 RRR 1294  
QY 417 tttagcag 476  
Db 1293 RRR 1234  
QY 477 atgag 536  
Db 1233 RRR 1174  
QY 537 acaactcaagaaataatcaagagagagagagagagagagagagagagagag 596  
Db 1173 RRR 1114  
QY 597 agaag 645  
Db 1113 RRR 1065  
RESULT 9  
AB029483 927 bp mRNA linear PLN 11-JAN-2001  
LOCUS AB029483  
DEFINITION Plasmid salkyvm cki mRNA for cyclin dependent kinase inhibitor,  
complete cds.

ACCESSION	AB029483
VERSION	AB029483.1 GI:12081914
KEYWORDS	Cyclin dependent kinase inhibitor.
SOURCE	Pisum sativum axillary bud cDNA to mRNA.
ORGANISM	Pisum sativum
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
REFERENCE	1 (bases 1 to 927)
AUTHORS	Shimizu-Sato, S. and Mori, H.
TITLE	AcNA, from Pisum sativum encoding the cyclin-dependent kinase inhibitor (CKI) homologue Published Only in Database (2001) In press
JOURNAL	2 (bases 1 to 927) Shimizu-Sato, S. and Mori, H.
REFERENCE	Direct Substitution Submitted (01-JUL-1999) Sae Shimizu-Sato, Nagoya University, Graduate School of Biological Sciences; Chikusa, Nagoya, Aichi 464-8601, Japan (E-mail:saesag@nagoya-u.ac.jp, Tel:+81-52-789-4166, Fax:+81-52-793-4296)
AUTHORS	
TITLE	
JOURNAL	
FEATURES	Location/Qualifiers
source	1..927
	/organism="Pisum sativum"
	/db.xref="taxon:3888"
	/tissue_type="axillary bud"
gene	51..629
	/gene="Cki"
CDS	51..629
	/gene="Cki"
	/codon_start=1
	/product="cyclin dependent kinase inhibitor"
	/protein_id="BAB20860.1"
	/db_xref="GI:12081915"
	/translation="MMAVGVRPARALAMPATSPRRTRKKIRNTENKFSYV KRIVTPEVTERRHSGSTSDPEEPASCCSNGLVEDRIRKISLDEVSAGFT SNQNDRIERERSRSFERSGSHLESMETSRFPSSPKRTTEVELEFFAAAE KDIOKRFQEKINVIDLDVPLEGRYEVOLKP"
BASE COUNT	299 a 163 c 211 g 254 t
ORIGIN	
	Query Match 8.3%; Score 75; DB 8; Length 927; Best Local Similarity 61.5%; Pred. No. 3.4e-05; Matches 120; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
OY	488 agatgtccacgaagaattcgaaattgtaagtatttttctgtgaagcgtgagaacaactcaag 547
Db	484 AGAGCGCCAGCAATCGAAGCTTGGAAGATTTCCTGCCTCGAGAAAAGACTTCACA 543
OY	548 aaattccaagaagaagtcacatttcgatatttcgagaagaagaccattagaagaagcgt 607
Db	544 AAAAATTTCAGAAAAAGTATAATTATGATATTCTGAAGAAGCGTTCCGTGGAAAGACGT 603
OY	608 acgaatcggttaaagcttagagctgaagaagaagaagaagctttaagttttttttaacct 667
Db	604 ACGAGTGGGTTCAGTTGAAGCCATTAACGCTGTGAACCTTTGCAATTGCCAC 663
OY	668 ttgaatttaataatt 682
Db	664 TTGCTGACATTTTT 678
RESULT 10	
LOCUS	AX008805 804 bp DNA linear PART 06-SEP-2000
DEFINITION	Sequence 15 from patent WO964599.
ACCESSION	AX008805
VERSION	AX008805.1 GI:9996264
KEYWORDS	. red goosefoot.
SOURCE	Chenopodium rubrum
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE		Spermatoxyphyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
AUTHORS		1 (bases 1 to 804)
TITLE		Fowke,L.C., Wang,H. and Crosby,W.L.
JOURNAL		Cyclin-dependent kinase inhibitors as plant growth regulators Patent: WO 964597-A 15 10-DEC-1995;
		FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV SASKATCHEWAN TECHNOLOGIES (CA)
FEATURES		Location/Qualifiers
SOURCE		1..804
BASE COUNT	254 a	/organism="Chenopodium rubrum"
ORIGIN	151 c 202 g 197 t	/db_xref="taxon:3560"
Query Match	8.0%; Score 72.4; DB 6; Length 804;	
Best Local Similarity	62.9%; Pred.No.0.00011;	
Matches 112;	Conservative 0; Mismatches 66; Indels 0; Gaps 0;	
Qy	462 ggaaggaagaaggcaattgatgcagggatcccaacggaatcggaattgaagtatttt 521	
Db	477 GGGGACCAATCATCACGTACAGATCAAAATCCCGTCGTGATTCAAATAATCGAATTTCTT 536	
Qy	522 ttgtgaagctcgaagaacaactcaagaagaataatcaagaagaagatcacatttcgattcga 581	
Db	537 TGTGTTTGCTGAAGAAAAGATCTCCAGAAGACGGCTCAGCGAAGAAAGTACATTTGCACATAGT 596	
Qy	582 gaagaggaagacccttctgaagagacgtttagaatggttaaagtttgagtggaagaagaaga 639	
Db	597 TTAAGACGTGCCACTGAAGAAGTGTGATTGATGTGGTTGCATTAATCATCATGATGATTAATA 654	
RESULT 11		
CRJ002173		804 bp MRNA linear PLN 27-MAY-1999
LOCUS		
DEFINITION	Chenopodium rubrum GI cyclin-dependent kinase inhibitor mRNA,	
ACCESSION	CRJ002173	complete cds.
VERSION	AJ002173.1	GI:2653280
KEYWORDS		cyclin-dependent kinase inhibitor.
SOURCE		red goosefoot.
ORGANISM		Chenopodium rubrum
REFERENCE		Ekaroyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodisceae; Chenopodium.
AUTHORS		1 (bases 1 to 804)
TITLE		Fountain,M.D., Renz,A. and Beck,E.
JOURNAL		Isolation of a cDNA encoding a Gi-cyclin-dependent kinase inhibitor from suspension-cultured photoautotrophic chenopodium rubrum cells Plant Physiol. 120, 339-339 (1999)
REFERENCE		2 (bases 1 to 804)
AUTHORS		Fountain,M.D.
TITLE		Direct Submission
JOURNAL		Submitted (25-NOV-1997) Fountain M.D., Plant Physiology, University Of Bayreuth, Universitaetsstrasse 30, 95447, GERMANY
FEATURES		Location/Qualifiers
SOURCE		1..804
		/organism="Chenopodium rubrum"
		/db_xref="taxon:3560"
		/clone="PBD-GAL4"
		/cell_type="photoautotrophic cells derived from hypocotyl tissue"
		/clone_11b="lamda hybridAP"
		/dev_stage="7 day old culture"
gene		58...648
CDs		/gene="CDK11"
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		/product="cyclin-dependent kinase inhibitor protein"
		/protein_id="CAA05215.1"

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/db_xref="GI:2653281"
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/translation="MAAATPTSSPAKKIKVYKSSYNTIPOLRRKKNLAPENFAEL
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AAVEKDLQKRESEKYNFDIVKDPVKRQDWVINP"
BASE COUNT      254 a      151 c      202 g      197 t
ORIGIN

Query Match      8.0%; Score 72.4; DB 8; Length 804;
Best Local Similarity 62.9%; Pred. No. 0.00011;
Matches 112; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 462 ggaaggaagcgcaaatgatgcagagatgcacaggaatcggaaattgaattttt 521
    || || || || || || || || || || || || || || || || || || || ||
DB 477 GGCGAGGAAATCAACGGTACAGATCAAGATCCGCTGATTCAGAAATCGAAGATCTT 536

QY 522 tctggaagctgagaacaactcaagaanaattcaagaagaattgacatttcga 581
    || || || || || || || || || || || || || || || || || || || ||
DB 537 TGGTGTGCTGAAAAAGATCTCCAGAAAGCGCTTCAGCGAAAGTACATTTGACATAGT 596

QY 582 gaaggaagacccattagagagacgtacgaatggtaagttagagtcgaagaaga 639
    || || || || || || || || || || || || || || || || || || || ||
DB 597 TAAAGACGTGCCACTGAAAGTCTGTATGATTGGGTTCCATTAATCCATGATATAA 654

RESULT 12
LOCUS      NTO297906      789 bp      mRNA      linear      PLN 03-OCT-2001
DEFINITION Nicotiana tomentosiformis mRNA for CDK/cyclin inhibitor (Kisla
            gene).
ACCESSION  AJ297906
VERSION     AJ297906.1 GI:15963347
KEYWORDS    CDK/cyclin inhibitor; Kisla gene.
SOURCE      Nicotiana tomentosiformis.
ORGANISM    Nicotiana tomentosiformis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanales; Solanales;
            1 (bases 1 to 789)
REFERENCE   1
  AUTHORS   Grandard,S., Perennas,C., Bernardi,F., Bergounioux,C. and Glab,N.
  TITLE     The tobacco CDK inhibitor NtKisla is involved in flower development
  JOURNAL   Unpublished
  AUTHORS   Grandard,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-Oct-2000) Grandard S., Science de la vie, CNRS,
            Universite, IBP, Universite Paris Sud, Bat 630, Orsay, 91405,
            FRANCE

FEATURES
  source      1..789      Location/Qualifiers
                /organism="Nicotiana tomentosiformis"
                /db_xref="taxon:4098"
                1..72
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                1..789
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                73..564
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                /product="CDK/cyclin inhibitor"
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                565..789
                /gene="Kisla"
                3'UTR      565..789
BASE COUNT      256 a      126 c      197 g      210 t
ORIGIN

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Query Match      7.7%; Score 69.4; DB 8; Length 789;
Best Local Similarity 66.2%; Pred. No. 0.00044;
Matches 100; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 486 ggaatgcacaggaatcgaatgaatgttttctgtgaagctgagaacactcaa 545
    || || || || || || || || || || || || || || || || || || || ||
DB 417 GAAATGCCGCTGAAAAAGAGATTGAAGATTTTTCAGCTGCCAGAAAGCTATACT 476

QY 546 agaaaattcaagaagaagtacatttcgatttcgaagaagaagcattagaagac 605
    || || || || || || || || || || || || || || || || || || || ||
DB 477 TAAACGATTTAAGAAAAAGTACACTTCGACTTGAAGAAAGAGGCAATGGAAGGTG 536

QY 606 ttacgaatggtaaggttagagttgaagaaga 636
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DB 537 CTACGAATGGGTCCGCAATAGGAAGTGAAGA 567

RESULT 13
LOCUS      AC091428      286564 bp      DNA      linear      HTG 20-APR-2001
DEFINITION Mus musculus chromosome 11 clone : MGS1-185K22, MGS1-180K15,
            MGS1-219P9, MGS1-6511L, *** SEQUENCING IN PROGRESS ***, 11
            unordered pieces.
ACCESSION  AC091428
VERSION     AC091428.1 GI:13699334
KEYWORDS    HTG; HTGS_PHASE1; HTGS_FULLTOP.
SOURCE      house mouse.
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
            1 (bases 1 to 286564)
REFERENCE   1
  AUTHORS   Resch,K., Platzer,M., Fuchs,S., Schlubel,M., Jockusch,H.,
            Rosenthal,A. and Schmitt-John,T.
  TITLE     Chromosome 11 genomic sequence
  JOURNAL   Unpublished
  AUTHORS   Platzer,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-Apr-2001) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
  COMMENT   * NOTE: This is a 'working draft' sequence. It currently
            * consists of 11 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.

            1
            12871: contig of 12871 bp in length
            * 12872
            12971: gap of unknown length
            * 12972
            62053: contig of 49082 bp in length
            * 62054
            62153: gap of unknown length
            * 62154
            253520: contig of 191367 bp in length
            * 253521
            253620: gap of unknown length
            * 253621
            258176: contig of 4556 bp in length
            * 258177
            258276: gap of unknown length
            * 258277
            263203: contig of 4927 bp in length
            * 263204
            263303: gap of unknown length
            * 263304
            267782: contig of 4479 bp in length
            * 267783
            267882: gap of unknown length
            * 267883
            277416: contig of 9534 bp in length
            * 277417
            277516: gap of unknown length
            * 277517
            279532: contig of 2016 bp in length
            * 279533
            279632: gap of unknown length
            * 279633
            282059: contig of 2427 bp in length
            * 282060
            282159: gap of unknown length
            * 282160
            284288: contig of 2129 bp in length
            * 284289
            284388: gap of unknown length
            * 284389
            286564: contig of 2176 bp in length.

FEATURES
  source      1..286564      Location/Qualifiers

```







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QY 571 ttctgatttcgagaaggagaag 591  
| |||||  
Db 217989 GAGAAGAGAGAGAGAAG 217969

Search completed: September 4, 2002, 18:25:33  
Job time: 9034 sec